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AX527916 LOCUS DEFINITION ACCESSION VERSION FEWENDES	AX527916 2881 bp DNA linear PAT 21-NOV-2002 Sequence 1 from Patent WO0229038. AX527916 AX527916.1 GI:25172359
SOURCE	Homo sapiens (human) Homo sapiens Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE AUTHORS TITLE	1 Herrmann,J.L., Rastelli,L. and Shimkets,R.A. Novel proteins and nucleic acids encoding same and antibodies directed against these proteins

10   10   10   10   10   10   10   10	1021 GGCTGGACTGCACTGGCGGAGCCGTGAGTGCTCTGACCCACCC	1081 GGGAGGA         1081 GGGAGGA	1141	1201 GCCTGGTCCTGCTTGTTCTCGTTTTTTTTGCGGAAGAAGGAGGGCTGG 1260	Y 1261 ACTCAGATGAGCTGACTCGTCCATTCTCAGCCTCAGGCTCCAGCCGTCAGCATCAAGC 1320	Y 1321 CCAGCAAAGCAGACAACCCCCATCTGCTCACCATCCAGCCGGACCTCAGCACCACCA 1380 b 1321 CCAGCAAAGCAGAAACCCCCATCTGCTCACCATCCAGCCGGACCTCAGCACCACCACCA 1380	Y 1381 CCTACCAGGCAGTCTCTGTCCCGGCAGGATGGCCCAAGTTCCAGCTCACA 1440 b 1381 CCTACCAGGCAGTCTCTGTCCCGGCAGGATGGCCCAAGTTCCAGCTCACA 1440	Y 1441 ATGGGCACCTGCTCAGCTGGCGGCCGCCACACTGCACCACAGCTCTCCCA 1500	1501   CTCTGAGGCCGAGGAGTTCGTCTCCCGCCTCTCCACCCAGAACTACTTCCGCTCCTGC 1560	1561 CCCGAGGCACCAGCAACATGACCTATGGGACCTTCAACTTCCTCGGGGGCCGGCTGATGA 1620	/ 1621 TCCCTAATACAGGTATCAGCCTCCTCATCCCCCGAATGCCATACCCGGAGGAAGATCT 1680 1621 TCCCTAATACAGGTATCAGCCTCCTCATCCCCCCAGATGCCCGGAGGGAAGATCT 1680	1681 AIGAGAICTACCTCACGCIGCACAAGCCGGAAGACGIGAGGTIGCCCCTAGCIGGCTGTC 1740	1741 AGACCTGCTGAGTCCCATCGTTAGCTGTGGACCCCCTGGCGTCCTGCTCACCCGGCCAG 1800	1801   TCATCCTGGCTATGGACCACTGTGGGGGGCCCTGACAGCTGGAGCCTGGCCTCA	1861 A 1861 A	1921 CCTCCCACCTCTACTGCCAGCTGGAGGCCAGTGCCTGCTACGTCTTCACCGAGCAGC 1980
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JOURNAL Patent: WO 0229038-A 1 11-APR-2002;  FEATURES Location (US)  SOURCE 1.2881  A.2881  A.299anism="Homo sapiens"  AD_xref="taxon:9606"	Query Match 100.0%; Score 2881; DB 6; Length 2881; Best Local Similarity 100.0%; Pred. No. 0; Matches 2881; Conservative 0; Mismatches 0; Indels 0; Gans 0;				Qy 181 CCAACCCAGTGCCTGGTGCCAACCGGACCTGCTTCCCACTTCTGGTGGAGCCCGAGG 240  Db 181 CCAACCCAGTGCCTGGTGCCAACCCGGACCTGCTTCCCACTTGGTGGAGCCGAGG 240	QY 241 AIGIGIACATCGTCAAGAACAAGCCAGTGCTGGTTGTGGAAGGCCGTGCCCGCCACGC 300  Db 241 AIGIGIACATCGTCAAGAACAAGCCAGTGCTTGTGTGCAAGGCCGTGCCGCCACGC 300	AGCGCA 	3GCAGC 4	4 4 8 8	ACTICG 54					84	

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  REFERENCE  AUTHORS  AUTHOR	Query Match         92.9%;         Score 2676.4;         DB 6;         Length 2752;           Best Local Similarity         98.9%;         Pred. No. 0;         9         Az ccGGGGGCCCGGCCCGCCCGCCCGCCCGCGCCCGCGCCATGGCCGTCCGCCC         3;           Qy         42 CCGGGGGCCCCGGCCCGGCCCGCCCGCCGCCGCGCCATGGCCGTCCGGCCC         101         AcGGGGGCCCGGCCCGGCCCGCCCGCCCGCCGCCGCCGCCG	Qy         162 CAGCAGAGTGCCACCGGGCCAACCCGGTGCCTAACCCGGACCTGCTTCCCCAC 221           Db         121 CAGCAGGTGCCACCGTGGCCAACCCGGACCTGCTTCCCCAC 180           Qy         222 TTCCTGGTGGACCCGAGCAGCTGCTTCCAACAACCAACCCGGTGCTGCTTCCCCAC 180           Db         181 TTCCTGGTGGAGCCGAGGATGTGTACATCGTCAACAACCAAC	Qy         402 ATTAATGTCTCAAGGCAGCAGCAGAAGGTGTTCGGGCTGGAGGAATACTGGTGCCAG 461           Db         361 ATTAATGTCTCAAGGCAGCTCGAGAAGGTTCGGGCTTGGAGGAATACTGGTGCCAG 420           Qy         462 TGCGTGGCATGAGCTCCTCGGGCACCACAGAGTCAGAAGGCTACATCCGCATAGCC 521           Db         421 TGCGTGGCATGAGACTCCTCGGGCACCACAGAGTCAGATCGCATAGCC 480           Qy         522 AGATTGCGCAAGAACTTCGAGCAGCACCACAGAGTCACATCCGCATAGCC 480           Db         481 AGATTGCGCAAGAACTTCGAGCAGGCCCTGGCCAAGAGTGCCCTGGAGCAGGCGAAGGCATGGCCATAGCC 480           Qy         522 AGATTGCGCAAGAACTTCGACGAGGAGCCGTGGCCAAGAGTGCTCCTGGAGCAGGCC 540           Db         481 AGATTGCGCAAGAACTTCGACCAGAGGCCCTCCAGCAGAGGCAGTGCCTCGGAGCAGGCCAGGGCAGGCCCTGGAGCCCTCCAGAGCAGTGCTCCTGGAGCAGTGCTCCTGGAGCAGTGCTCCGGGGAGTGGAGTGGCTCCGGGGAGTGGAGTGGCTCCGGGGAGCAGTCCCTCCAGCCGAGAGTGGAGTGGCTCCGGGGGAGCTCCTCCAGCCGGAGGGCAGTGGAGTGGCTCCGGGGGAGCCTCCTGGAGCCCTCCTCCAGCCGGAGGGCAGCTCCCTCGGAGCTGGCTCCCTGGAGCCCTCCTCCAGCCGGAGGGTGGAGTGGCTCCCGGGGGAGCCTCCTCGAGCCCCTCCAGCCGGAGGCCTCCCTGGAGCCCCTCCAGCCGGAGGCCTCCCTGGAGCCCCTCCAGCCGGGAGGCTCCCTCGGGGGAGCCCTCCGGGGGGGG	QY         702 CTGGTGGTGCACAGGCCGCTTGCTGACACGCCAACTACACCTGCGTGGCCAAGAAC 761           Db         661 CTGGTGGTGGACAGGCCCGCCTTGCTGACACGCCAACTACACCTGCGTGGCCAAGAAC 720           QY         762 ATCGTGGCACGTCGCCGCACCTCCGCTGCTGCTTCGTCTACGTGAACGGTGGGTG
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JOURNAL Patent: WO 0233080-A 1 25-APR-2002;  FATURES Location/Qualifiers Source 1.2697 Organism="Homo sapiens" /wol_type="unassigned DNA" /db_xref="taxon:9606"  Query Match 90.8%; Score 2615; DB 6; Length 2697; Best Local Similarity 98.7%; Pred. No. 0; Matches 2669; Conservative 0; Mismatches 25; Indels 9; Gaps 3;		207 GACCTGCTTCCCCACTTCTGGTGAGCCCGAGGATGTGTACATCGTCAAGAACAAGCCA  207 GACCTGCTTCCCCACTTCTGGTGAGCCCGAGGATGTGTACATCGTCAAGAACAAGCCA  121 GACCTGCTTCCTGGTGAGGCCCGAGGATGTGTACATCGTCAAGAACAAGCCA  267 GTGCTGCTTGTGGAGCCGTGCCCGCCAGATCTTCTAAGTGCAACGGGAG  181 GTGCTGCTTGTTGTGAAGACCGTGCCCGCCAAGATCTTCTTCAAGTGCAACGGGAG  181 GTGCTGCTTGTTGTAGAAGCCGTGCCCGCCAAGATCTTCTTCAAGTGCAACGCCAA	327 TGGGTGCGCCAGGTGGACCACGTGATCGAGCGCAGCACAGACGGGAGTGGTGAGCCG 38  [	301 ACCATGGAGGTCCGCATTAATGTCTCAAGGCAGCAGGAGGTCGAGAAGGTGTTCGGGGCAGAGGTCGAGAAGGTGTTCGGGGCAGGGGGGGG	Db   421 TACATCGGCATAGCCTATTTGCGCAAGAACTTCGAGCAGGAGCGCGAAGGGGTG 480	541 GTGGAGTGGCTCCGGAACGAGGACCTGGTGGACCCGTCCTGGACCCCATGTTTTTTTT	Db   661 TGGGTGGCGAĞAACATGGTGGCGGĞGGGCGTCGGTGTCATGGTCTTC 720     Qy   807 GTGAACGGTGGTGGTCGACGGGGGCGCTGCTGCAGCGCCGGTGTGGGCGC 866

source 13580 /organism="Homo sapiens" /mol_type="unassigned DNA" /db xref="taxon:9666" /note="Incyte ID No: 6052371CB1"	Query Match Best Local Similarity 93.4%; Score 2402.6; DB 6; Length 3580; Best Local Similarity 93.4%; Pred. No. 0; Matches 2615; Conservative 0; Mismatches 9; Indels 177; Gaps 3;	QY         84 GCCATGGCCGCTCGGCCTGTGGCCACGCCTCCTGGGCATAGTCCTCGCCGCTTGG         143	0y 144 CTCCGCGGCTCGGGTGCCCAGAGTGCCACCGTGGCCAACCCGGTGCCTGGTGCCAAC 203	OY 204 CCGGACCTGCTTCCCCACTTCCTGGTGGAGCCCGAGGATGTGTACATCGTCAAGAACAAG 263	OY 264 CCAGTGCTGCTTGTGTAAGGCCGTGCCCGCCACGCAGATCTTCTTCAAGTGCAACGGG 323	OY 324 GAGTGGGCCAGGTGGACCACGTGATCGAGCGCAGCACAGGGGAGCAGTGGTGG 383	OY 384 CCGACCATGGAGGTCCGCATTAATGTCTCAAGGCAGCAGGAGGAGGTCGAGAAGGTGTTCGGGCTG 443	OY 444 GAGGAATACTGGTGCCAGTGCATGCATCCTCGGGCACCACCAAGAGTCAGAAG 503	OY 504 GCCTACATCGCATAGCCAGATTGCGCAAGAACTTCGAGGAGCCGCTGGCCAAGGAG 563	0y 564 GIGICCCTGGAGGGCAICGTGCTCCCTGCCGTCCACCGAGGGCAICCCTCCAGCC 623 	0y 624 GAGGTGGAGTCCGGAACGAGGACCTGGTGGACCCGTGGACCCCATGTATAC 683 	0y 684 ATCACGCGGAACACACAGTGGTGCGACAGGCCCGCTTGCTGACACGGCCAACTAC 743	QY         744 ACCTGGGGGCCAGAACATGGTGGCAGGTGCTGCTGCTGTTGTTC         803           Db         661 ACCTGGGTGGCCAAGAACATGGTGGCACGCGCAGCGCTTCGTTCG	804 TACGTGAACGGTGGGTGGACGTGGACCGAGTGGTCCGTCTGCAGCGCCAGCTGTGGG	Db 721 TAC 723 OV 864 CECECTER DA DE	724	OY 924 TICTGTGAGGGCAGAATGTCCATGACCGCACCGTCTCTCTTGCTTG	984 GGCAGCTGGAGCCCGTGGAGCAAGTGGTCGGCCTGTGGGCTGGACTGCACTGGCGG
	QY 2184 CIGCACHICAAGGACAGTTACCACAACCIGCGCCTATCCATCAGGATGTGCCCAGGTCC 2243	Qy 2244 CTGTGGAAGAGTAAGCTCCTTGTCAGCTACCAGGAGATCCCCTTTTATCACATCTGGAAT 2303	OY 2304 GGCACGCAGTACTTGCACTTCACCTTGAAGGTGTGTCAGCCCCAGCACTAGT 2363	Qy         2364         GACCTGGCCTGCAAGCTGTGGCAGGCAGGCGAGGCGACGGCAGAGCTTCAGCATC         2423           Db         2275         GACCTGGCCTGCAGAGCTGTGGCAGGTGGAGGCGACGGCCAGAGCTTCAGCATC         2334	OY 2424 AACTICAACAICACCAAGGACACAAGGIITIGCIGAGCTGCTGGCTCTGGAGAGTGAAGCG 2483  Db 2335 AACTICAACAICACCAAGGACACAAGGTTTGCTGAGCTGCTGGAGAGTGAAGCG 2394	OY 2484 GGGGTCCCAGCCGGGCCCCAGTGCCTTCAAGATCCCCTTCTCATTCGGCAGAAG 2543	Qy 2544 ATRANTITCCAGCCTGGACCCACCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAG 2603  [	OY 2604 AAACTCCACCTGGACAGCCATCTCAGCTTCTTGCCTCCAAGCCCAGCCCACAGCCATG 2663	OY 2664 AICCICAACCIGIGGGAGGCGCGCACTICCCCAACGGCAACCICAGCCAGCTGGCTGGC 2723	Qy         2724         GCAGTGGCTGGACTGGCCAGCCAGCCTTCACAGTGTCGAGGCTGAGTGC         2783           L	Oy 2784 TGA 2786  Db 2695 TGA 2697	T 4 094	LOCUS  LOCUS  AX36/1094  SSB0 bp  DNA  Innear PAT 16-FEB-2002  ACCESSION  AX367094.1 GI:18855296			AUTHORS Griffin, J.A., Kallick, D.A., Tribouley, C.M., Yue, H., Nguyen, D.B., Tang, Y.T., Lal, P., Polick, J.L., Azimzai, Y. Luu, D., Graul, R.,		JOURNAL Patent: WO 0198354-A 13 27-DEC-2001; JOCYTE Genomics, Inc. (US) FEATURES Location/Qualifiers

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1917   CTCAAGGAGGTGGTGCACCTGGAGAAGCTGGGGGGACACCTGATCCACGAGCCACGG 1926	MANUA87852 LOCUS MANUA87852 LOCUS MANUA87852 MANUA87852 DEFINITION MAGE musculus mRNA for netrin receptor Unc5h1 (Unc5h1 gene). ACCESSION MAGE musculus (Nouse mouse) ORGANISM MUSCULUS ELKEYWORDS SOURCE MUSCULUS GRANISM MUSCULUS GRANISM MUSCULUS FURATYOTA; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; MAMMATIA; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus. AUTHORS TITLE AUTHORS Cloning of three mouse Unc5 genes and their expression patterns at mid-gestation JOURNAL Mech. Dev. 118 (1-2), 191-197 (2002) MEDLINE 22239710 PUBMED 12351186 REFERENCE 2 (bases 1 to 3992)
1044   AGCOCTGAAGCCCGTGAAGCAAGTGGTCGGCCTGGGGCTGGACTGCCCCAACTGGCCGG	1821   TGTGGGGGGCCCGGCCTGACAGCTGGGGCCTCAAAAAGCAGTCGTGCGAGGC   1880

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CTGCCCCGAGGCACCAGCAACATGACCTATGGGACCTTCAACTTTCCTCGGGGGCCGGCTG 1616
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DVADSSILTGGFOPVSIKPSKADNPHLLTIOPDLSTTTTTYGGSLCPRODGSPEPKEGL
SNGHLLSEPLGSCRHTLHKSSPYSBAEDRYSKLSTQNYFRSLPRGTSNNAYGFINFLGG
RIMI PNYGISLLIPPDALPRGKLYEIYLTHKPEDVRLAFACOCTLLSPIVSCGPPGV
LITREVILLARDHCGEPSPSSWSLELKYKOGSCGSWEDVHLGESESPSHLYYCQLEAGAC
YCFTEGLGREALSVAATKRLALLEAPVACTSLEXNIRVYCLHDTHDALKEVY
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YICVAKNIVARRRSASAAVIVYVNGGNSTWTEMSVCSASCGRGWQKRSRSCTNPAPLN
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.larity 89.3%; Pred. No. 0;
Conservative 0; Mismatches 292; Indels 16;
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Direct Submission
Submitted (15-MAY-2002) Neuroanatomy,
                                                                                                           organism="Mus musculus"
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232. .2928
/gene="Unc5h1"
/codon_start=1
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                      ATAATTTCCAGCCTGGACCCACCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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llarity 88.9%; Pred. No. 0;
Conservative 0; Mismatches
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/organism="Rattus sp."
/mol_type="unassigned DNA"
/db_xref="taxon:10118"
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by 2544 ATAATTTCCAGCTGGACCCACCTGTAGGGGGGTGCCGACTC	2604	2575	Db 2635 GCTGTGGCCGGACTGGGCCGACCAGGCTGCGCTTTTCACGGGCCGACCAGATGCTGGCCTTTTCACGGGCCGACCAGATGCTGGCCTCTTCACGGGCCGACCAGATGCTGGCCTCTTCACGGGCCAACCAGATGCTGGCCTCTTCACGGGCCAACCAGATGCTGGCCTCTTCACGGGCCAACCAGATGCTGGCCTCTTCACGGGCCAACCAGATGCTGGCCTCTTCACGGGCCAACCAGATGCTGGCCTCTTCACGGGCCAACCAGATGCTGGCCTCTTCACGGGCCAACCAGATGCTGGCCTCTTCACGGGCCAACCAGATGCTTCACGGGCCAACCAGATGCTTCACGGGCCAACAGATGCTTCACGGGCCAACAGATGCTTCACGGGCCAACAGATGCTTCACGGGCCAACAGATGCTTCACAGATAGAT	2695 TGA	RESULT 8 RNU87305 LOCUS LOCUS RATUS RATUS NORYGICUS transmembrane receptor Unc5	U87305.1 GI:2055391 Battus norvegicus (Norway rat.)	ANISM Rattus norvegicus Eukaryota, Metazoa, Chorda Mammalia, Eutheria, Rodeni	REFERENCE 1 (Dases 1 to 2697) AUTHORS Leonardo, E.D., Hinck, L., Masu, M., Keino-Masu, Tessier-Lavigne, M. TITLE Vertebrach homoloques of C. elegans UNC-5 are	receptors AL Nature 386 (6627), 833-838 (1997) NE 97271897	REFERENCE 2 (bases 1 to 2697) AUTHORS Leonardo, E.D., Hinck, L., Masu, M., Keino-Masu, Tessier-Lavigne, M. TITLE Direct Submission	ALS	/organism="Rattus norvegicus" /mol_type="mRNA" /db xref="taxon:10116" /+iceue tyme="hypain and yentral	/dev stage="18 day embyo and 13 day 1. 2697 1. 7690 statt=1 /cooding tart=1	/protein id="Amb57678.1" /protein id="Amb57678.1" /db_xref="G1:205392" /translation="MAVRPGLWPVILGIVLAAWIRG #FINRERPHYVINKRYRVII.NCKAVPATOIFFKCNGE	EVALINVSROQVEKYFGLEEYWCCVVAWSSGGTTKSQ BYLEQGIVLECRPPEGLEPAEVEWLANEDLYDPSLIDP YTCVAKNI VARRSGTSAAVIVYNGGWSTWTEWSVC GGAFCEGONVOKTACATLCPVDGGWSSWGSKACE	RGADLDTRNCTSDLCLHTASCPEDVALYIGLVAVAV DVADSSILTSGROPVSIRKSKADNPHLLTIQPDLST SNGHLLSPLGSGRHTLHHSSPTSEAEDFVSRLSTON RIMI PNTGISLI I PPDAIPRGK YEI YLTHKPEDV	LLTRPVILAMDHCGEPSPDSWSLRLKKQSCEGSWEI YVFTEQLGRFALVGEALSVAATKRLRLLFRAPVACT QLEKQLGGQLIQEPRVLHFKDSYHNLRLSIHDVPSS QQYLHCTFTLERINASTSDLACKVWVWQVEGDGQSF
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TYKSQQQXYIR IAYLRKPEQPPLAKEV
TYKSQQXYIR IAYLRKPEQPPLAKEV
SELDPWYITREHSLVVRQARLADTAN
WSVCSASCGROWQKRSRSCTNPAPLIN
ANGALDCTHWRSRECSDPAPRNGGEEC
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STQNYRSRELPRTSNMAYCFTNFLGG
FEBDVRLLLAGCOTLLSPVVSCGPPGV
SWEDVLLIGESPSHLYYCQLEAGAC
VYACTSLEYNIRYCLHPHALKEV
VYACTSLEYNIRYCHNFLOALGS
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VQQSFNINFNIRYCHTREALLALESEG AGTGTCGGAGGCTGAGTGC 2783 TIGGCGGACTCTGGCCCAG 2603 CTCGGCCAGCTGGCAGCA 2634 linear ROD 15-MAY-1997 c5H1 mRNA, complete cds. CTCAGCCAGCTGGCTGCA 2723 SCCCAGCCCACAGCCATG 2663 1, K., Ackerman, S.L. and tebrata; Euteleostomi; Muridae; Murinae; re candidate netrin Parnassus, San oinal cord" ay embryo" u, K. and NC5H1"

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ORIGIN	GVPALVGPSAFKI PFLIRQKI IASLDPPCSRGADWRTLAQKLHLDSHLSFFASK AMILNLWEARHFPNGNLGQLAAAVAGLGQPDAGLFTVSEAEC"
Query Best ] Match	rry Match 16.0%; Score 2189.4; DB 10; Length 2697; st Local Similarity 88.9%; Pred. No. 0; ches 2403; Conservative 0; Mismatches 291; Indels 9; Gaps
λ	TGGCCAGCGCTCCTGGGCATAGTCCTCGCCGCTT
ΩÞ	CGGCCTGTGGCCAGTGCTCCTGGGCATAGTCCTCGCCGCC
οχ	AACCCAGTGCCTGGTGCCAAC
qq	CCAGCAGAGTGCCACGGTGG
δy	GA.
qq	121 GACCTGCTCCCCCACTTCCTGGTAGAGCCTGAGGACGTGTACATTGTCAAGAAGACGCG
ò	267 GIGCTGTGTGTGCAAGGCGTGCCGCCACGCAGATCTTCTTCAAGTGCAACGGGAG
DP	181 GIGITGITGGTGTGCAGGCTGTGCCTGCCACCCAGATCTTCTTCAAGTGAATGGGGAA
à	327 TGGGTGCGCCAGGTGGACCACGTGATCGAGCGCACACACA
qq	241 TGGGTCCGCCAGGTCGATCACGTAATTGAACGCAGCACCGACGGCAGCGGATTGCCA
λŏ	387 ACCATGGAGGTCCGCATTAATGTCTCAAGGCAGGTCGAGAAGTGTTCGGGTGGAG
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ζζ	GGGGCACCACCAAGAGTCAGAAGGC
Db	361 GAATACTGGTGCCAGTGTGTGGCATGGAGCTCCTCGGGTACCACCAAAAGTCAGAAGGCC
ά	507 TACATCCGCATAGCCAGATTGCGCAAGAACTTCGAGCAGGAGCCGCTGGCCAAGGAGGTG
đa	421 TACATCCGGATTGCCTATTTGCGCAAGAACTTTGAGCAGCGCCCCTGGCCAAGGAAGTG
ογ	567 TCCCTGGAGCAGGCATCGTGCTGCCCTGCCGTCCACGGAGGCATCCTCCAGCGAG
qa	481 TCACTGGAGGAAGGCATTGTACTACCTTGTCGCCCCCCAGAAGGAATCCCCCCAGCTGAG
ò	627 GTGGAGTGGCTCCGGAAGACCTGGTGGACCCGTCCCTGGACCCCAATGTATACATC
QQ	541 GIGGAGIGGCTTCGAAATGAGGACCTCGTGGACCCCTCCCTCGATCCCAATGTGTGACCT
λö	SACACGGCCAACTACAC
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δλ	747 TGCGTGGCCAAGAACATCGTGGCACGTCGCCGCAGCGCCTCCGCTGCTGTCATCGTCTAC
QQ	CAAGAACATCGTAGCCCGTCGCCGAAGCA
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QQ	GTCTGCAGCGCCAG
δλ	867 GGCTGGCAGAACGGAGCCGGAGCTGCACCCGGCGCCTCTCAACGGGGGCGCTTTC
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δλ	927 TGTGAGGGGCAGAATGTCCATGACGGCACCGTCTCCTCTGCTTGTCTCTGGACGGC
DÞ	841 TGTGAGGGCAGAATGTCCAGAAAACAGCCTGCGCCACTCTGTGCCCAGTGGG 8
δλ	GCTGGAGCCCGTGGAGCAAGTGGTCGGCCTGTGGGCTGGACTGCACCCACTGGCGGGG
qq	898 AGCTGGAGTTCGTGGAGTAAGTGGTCAGCCTGTGGGGCTTGACTGCACCCACTGGGGAGC
Qy	1047 CGTGAGTGCTCTGACCCCAGCACCCCGCAACGGGGGGGGG

GACACCGGCAACTGTACCAGTGACCTCTGTACACAGTGCTTCTGGCCCTGAGGACGTG GACACCGGAACTGTACCAGTGACCTCTGCCTGCACACGCTTCTTGCCCCGGAGGACGTG GCCCTCTATGTGGGCCTCATCGCCGTGGCCGTCTGCTGCTGCTGCTGCTTGTCCTC GCTCTCTACATCGGCCTTGTGTGTGTGTGCCTCTTCTTGCTGTGGCCCTT ATCCTCGTTTATTGCCGGAAGAAGAAGGGGCTGGACTCAGATGTGGCTGACTCGTCCATT GGACTCATTTACTGTCGCAAGAAGGAAGGACTGGACTCCGATGTGGCCGACTCGTCCATC CTCACCTCAGGCTTCCAGCCCGTCAGCATCAAGCCAGCAAAGCAGAACCCCCATCTG CTCACCTCGGGCTTCCAGCCTGTCAGCATCAAGCCCAGCAAAACAACCCCCACCTG CGGCAGGATGGGCCCAGCCCCAAGTTCCAGCTCACCAATGGGCACCTGCTCAGCCCCCTG AGGCAGGATGGACCCCCAAGTTCCAGCTCTCTAATGGTCACCTGCTCAGCCCACTG GGTGGCGCCCACACACACACCACACCTCCCACCTCTGAGGCCGAGGAGTTCGTC TCCCGCCTCTCCACCCAGAACTACTTCCGCTCCCTGCCCCGAGGCACCAGCAACATGACC CTCATCCCCCCAGATGCCCATACCCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCAC CTGGAGGCCAGTGCCTGCTACGTCTTCACCGAGCAGCTGGGGCCCCTTTGCCCTGGTGGAACTGGGAGCCGCTTTGCCCTGGTAGGACCGGGGGCCGGCTTTGCCCTGGTAGGA TATGGGACCTTCAACTTCCTCGGGGGCCGGCTGATGATCCTTAATACAGGTATCAGCTC **AAGCCGGAAGACGTGAGGTTGCCCCTAGCTGGTGAGACCCTGCTGAGTCCCATCGTT** AAGCCAGAAGACGTGACGTTGCCCCTAGCTGGTGAGACCCTGCTGAGTCCAGTCGTT AGCTGTGGACCCCTGGCGTCCTGCTCACCCGGCCAGTCATCGTGGACGACTGT GGGGAGCCCAGCCTGACAGCTGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGGAGCAGC TGGGAGCAGGATGTGCTGCACCTGGGCGAGGAGGCGCCCTCCCACCTCTACTACTGCCAG GAGGCCCTCAGCGTGGCTGCCGAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCC AAGGAGGTGCAGCTGGAGAAAGCAGCTGGGGGGAACAGCTGATCCAGGAGCCACGGGTC KPSPT ų. B40 

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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 23346570.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GVLLTRPVILAMDHCGEPSEDSWSLRLKKQSCEGSWEDVLHLGEESPSHLYYCQLEAG
ACYVFTBQLGRFALVGEALSVAATKRLRLLLPAPVACTSLEYNIRVYCLHDTHDALKE
VVQLEKQLGGQLIQEPRVLHFKDSYHNLRLSIHDVPSSLWKSKLLVSYQEIPFYHIWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Letticia Helato, Martin Krzywinski, Reta Kutsche, Ollver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Lilsa Prabhu, Parvaneh Saedi, Jacqueline Schein, Duane Smallus, Michael Smitht, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Sakalska, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A. Goldin, J.E., Jones, S.J. and Marra, M.A. Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (08-SEP-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue type="Brain, mouse, 13.5, 14.5, 16.5, 17.5 dpc"/clone lib="NIH BMAP_FW0"
/lab host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of Iowa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library Preparation: M. Bento Soares, University of Iowa Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
                                                                                                                                                                                                                                                                 human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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/clone="MGC:66671 IMAGE:6813463"
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/db_xref="Gl:34784159"
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/db_xref="LocusID:107448"
/db_xref="MGI:894682"
252. .2780
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/mol type="mRNA"
/strain="C57BL/6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Vector: pYX-ASC"
                                                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 3844)
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AUTHORS
TITLE
JOURNAL
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COMMENT
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E. (bases 1 to 2844).

Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.L., Colling,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Deducliano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Morley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Mazny,D.M., Sodeegren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
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                                                                                                                                                                                                                                                                                                                                                      creregaadacaactrorcactractacadaaarcccrrrrraccacarcregaac 2214
                     AAGGAGGTGGTGCAGCTGGAGAAGCAGCTAGGTGGACAGCTGATCCAGGAGCCTCGCGTC 2094
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2604 AAACTCCACCTGGACAGCCATCTCAGCTTCTTTGCCTCCAAGCCCCACAGCCATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2424 AACTICAACAICACCAAGGACACAAGGITIGCIGAGCIGCIGGCICIGGAGAGIGAAGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGGGTCCCAGCCCTGGTGGCCCCAGTGCCTTCAAGATCCCCTTCCTCATTCGGCAGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2544 ATAATTICCAGCCTGGACCCACCTGTAGGCGGGGTGCCGACTGGCGGGCTTGGCCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2215 GGCACCCAGCAGTATCTGCACTGCACCTCACCCTGGAGCGCATCAACGCCAGCAGCACCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2275 GACCTGGCCTGCAAGGTGTGGGTGTGGCAGGTGGGGGAGAGTGGGCAGAGTTGACATC
                                                                                                                                                                                        crecacricaaagacagiraccacaaccrecircicriccarccacgacgigcaccicc
                                                                                                                                                                                                                                                                                                                                                                                                                                        GGCACGCAGCGGTACTTGCACTTCACCCTGGAGCGTGTCAGCCCCAGCACTAGT
                                                                                                               musculus (house mouse)
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AUTHORS
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720 CGCCTTGCTGACACGGCCAACTACACCTGCGTGGCCAAGAACATCGTGGCACGTCGCCGC 779	960 ICCTCTCTGCTTGTCTGTGGACGGCAGCTGGAGCCCGTGGAGCAAGTGGTCGGCCTGT 1019	1080 GGGGAGGAGTGCCAGGGCACTGACCTGGAACTGTACCAGTGACCTCTGTGTA 1139	1200   TGCCTGGTCCTGCTGCTTGTCCTCGTTTATTGCCGGAAGAAGGAGGGGCTG   1259	1310   CCCAGCAAAGCACAACCCCCATCTGCTCAGCCGGGACCTCAGCACCACC	1437 ACCAATGGGACCTGGTCAGCCCCTGGGCGGCCGCCACACTGCACCACAGCTCT 1496  1434 TCTAATGGTCACCTGGTCAGCCCACTGGGCGCCCATACGCTGCACCACCAGCTCC 1493  1497 CCCACCTCTGAGGCCGAGGAGTTCGTCTCCCGCCTCTCCACCCAGAACTACTTCCGCTCC 1556	16	
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GTQOYLHCTFTLERVNASTSDLACKVWWQVEGDGQSFNINFNITKDTRFABMIALES EGGYPALVGESAFKIPFLIRQKIITSLDPPCSRGADWRTLAQKHLDSHLSFFASKPS  Misc_feature	Some (but not all) of these domains form homotypic and heterotypic dimers."  /db_xref="CDD:smart00005"  Query Match 70.1%; Score 2020.6; DB 10; Length 3844;  Best Local Similarity 84.1%; Pred. No. 0;  Matches 2429; Conservative 0; Mismatches 274; Indels 184; Gaps 6;	390GCT - AAAGCCGCCCCGCGCGGGGGCCCCGCGCC 59   390GCTGCCGCCCGCGCGGGGGCCCCTAGTC					

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Strausberg, L. (Dates I to Cabes 
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Series: IRAL Plate: 26 Row: g Column: 22.
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Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,

Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,

Blakesley, R. W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,

Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,

Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R.,

Maduro, Q.L., Mastello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,

McCowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W.,

Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,

Young, A., Zhang, L.-H., and Green, E.D.
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                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2688)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (12-JUN-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL.)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
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On Dec 19, 2003 this sequence version replaced gi:14424611.
Contact: MGC help desk
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/note="ZU5; Region: Domain present in 20-1
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/tissue type="Brain, neuroblastoma"
/clone_lib="NIH_MGC_19"
/lab_host="DH10B-R"
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1343. .1594
/note="DEATH, Region: DEATH domain, involved in Cell death (apoptosis)"
/db_xref="CDD:smart00005"
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/product="Unknown (protein
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QY         2670 AACCTGTGGGAGGCGCGCACTTCCCCAACGGCAACCTCAGCCAGC	RESULT 12 AX054976 LOCUS LOCUS LOCUS LOCUS Sequence 91 from Patent W00073328. AX054976 AX064976 AX0649	Query Match         44.8%; Score 1291.2; DB 6; Length 9700;           Best Local Similarity         99.5%; Pred. No. 9e-204;           Matches 1306; Conservative         0; Mismatches         3; Indels         3; Gaps         1;           QY         1478 CACACTGCACCACACTCTCCCACCTCTGAGGAGTTCGTCTCCCGCCTCTCCAC         1537           Db         7 CACACTGCACCACACTCTCCCACCTCTGAGGACTCTCCCGCCTCCCACGAGGAGTTCGTCTCCCACCTCTCCACCTCCCGAGGAGCTCTCCACCTCCCACCACACATCGCTCCTCCACCTCCCCACCACACATCGCTCCTCCACCTCCACCACACATCACTCTCCCCCACACACACATCACCTCTCCAACACACACACACACACACACACACACACACACACACA	QY         1718 GAGGTTGCCCTAGCTGGTGAGACCCTGCTGAGTCCCATCGTTAGCTGTGGACCCCC         177           Db         247 GAGGTTGCCCCTAGCTGGCTGTCAGACCCTGCTTAGCTTGGACCCCC         306           QY         1778 TGCGTCCTGCTCACCCGGCCAGTCATCCTGGCTATGGACCACTGTGGAGCCCAGCCC         1837           Db         307 TGGCGTCCTGCTCACCCGGCCAGTCATCCTGGCTATGGACCACTGTGGGAGCCCAGCCC         366           QY         1838 TGACAGCTGGAGCCTCAAAAAGAACAACCAGTGGAGGCCACTGTGGGAGCCAGCC

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PFHELPETFPSDPPFEPLPHFLIEPEBAYIVKNKPVNLYCKASPATQIYFKCNSBWVHQ
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RIAYLRKTFEQEPLGKEVSLEQEVLLQCRPPEGIPVAEVEWLKNEDIIDPAEDRNFYI
TIDHNLIIKQARLSDTANYTCVAKNIVAKRKSTTATVIVYVNGGWSTWTEWSVCNSRC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       487
                                                                                                                                                                                        2 (bases 1 to 9299)
Ackerman, S.L., Kozak, L.P., Rund, L.A. and Knowles, B.B.
Direct Submission
Submitted (25-SEP-1996) The Jackson Laboratory, 600 Main Street,
Bar Harbor, ME 04609, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tcaagtgcaacagcgagtgcgttcarcagaaggaccacgragtagagagagagagagagaga
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               Boyer, B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  product="rostral cerebellar malformation protein'
                                                                an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 10; Length 9299;
               Rund, L.A.,
                                                                mouse rostral cerebellar malformation gene encodes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="similar to C. elegans UNC-5"
               Przyborski, S.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               function="transmembrane receptor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 940.2; DB 10;
Pred. No. 9.9e-146;
0; Mismatches 943;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               map="between Amy1 and Mpmv9"
L. 9299
'gene="rcm"
                                                                                                                                                                                                                                                                                                                                                    /organism="Mus musculus"
/mol type="mRNA"
ferrain="C57B6/SJL"
/db xref="taxon:10090"
/chromosome="3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein_id="AAB54103.1"
db_xref="G1:2088527"
                                                                                       UNC-5-like protein
Nature 386 (6627), 838-842 (1997)
97271898
                 Kozak, L.P.,
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/gene="rcm"
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hes 1642; Conservative
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                    Ackerman, S.L., Ko
and Knowles, B.B.
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AUTHORS
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PUBMED
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 $\delta$ g ò g à g ð qq  $\delta$ d ð Db  $\overset{\circ}{\circ}$ P ò Ωp  $\delta$ Db ò g  $\delta$ qq

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GREPOKRTRTCTNPAPLINGGRECEGONVOKTACTTLCPVDGKWTSWSKWSTCGTECTH
WRRBECTAPAPKNGGKDCEGLVLQSKNCTDGLCMQAAPDSDDVALYVGIVIAVUVCLA
ISVVVALFVYRKNHRPRESDIIDSAALMGREPQPVNIKRARQDLLAVPPDILTSAAAMYR
GPVYALHDVSDKIPWTNSPTLDPLENLKIKYNTGGAVTPQDELSDFSSKLSPQITQS
LLENBTLAVKNQSLARQTDPSCTAFGTFNSLGGHLVIPNSGVSLLIPAGAVPQCRVYE
MYVTPHREGMREPVEDSQTLIPPVSCGPPCALLTRPVVLTMHGAERNEDMOJQL
KHOAGOGPWEDVVVVGEENFTTPCYIQLDPEACHILTFTLSTYALVGGSITKAAAKRL
KLAIFGPLSCSSLEYSIRVSCKLPAKYGLDDTQDAALKEVAGGILEEPRTHFKGSTHN
LRLGIHDIAASLWKSKLPAKYGLDPTQDAALKEVAGGILEEPRTHFKKSTHN
LRLGIHDIAASLWKSKLPAKYGLIPPYHINSGCQRNHHCTFTLERFSLNTLEFLVCKLC
VRQVEGEGQIPQLNCSVSEEPTGIDYPIMDSAGSITTIVGPNAPSIPLERYGKLCSSL
DAPQTRGHUNRMLAAHKLAKDRXLAVFATKSSPTGVILDLWEAQNFPDGNLSNLAAVULE
EMGRHETVVSLAABGNY"
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PFHELPETPESDPPEPLPHFLIBPEEAXIVGKPVMLXCKASPATQIYFKCNSEWVHQ
KDHVVDRFYDESDPTSGLIVCHSVEISRQOVEELFGPEDYWGCOVAMSSAGTTKSRKAYV
RIAYLKOFRTPGQPFOKSEVSKLSQEVLLQCRPPEGIPVABVEWLKNEEVIDPVEDRNFYI
TIDHNLIIKQARLSDTANYTCVAKNIVAKRKSTTATVIVYVNGGWSTWTEWSACNSRC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.

E 1 (bases 1 to 2962)

S Guan, W. and Condic, M.L.
Characterization of Netrin-1, Neogenin and cUNC-5H3 expression
during chick dorsal root ganglia development
Gene Expr. Patterns 3, 369-373 (2003)

S Guan, W. and Condic, M.L.
Direct Submission

L Submitted (26-NOV-2002) Neurobiology & Anatomy, University of Utah,
20 North, 1900 East, Salt Lake City, UT 84132-3401, USA

L Direct Submission

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Euteleostomi;
TGGCCCATAAACTCAACCTGGACAGGTACTTGAATTACTTTGCCACCAAATCGAGCCCAA
                                                                                                                                                                                                                      TGGCTGCAGCAGTGGCTGGACTGGGCCAGCCAGCGCTGGCCTCTTCACAGTGTCGGAGG
                                                                                                                                    CTGGCGTAATCCTGGATCTTTGGGAAGCACAAACTTCCCAGATGGAAACCTGAGCATGC
                                                                                                                                                                                                                                                                                                    TGGCAGCCGTCCTGGAAAAATGGGAAGACATGAGACAGTGGTGTCCTTGGCAGCAGAAG
                                                                          TGCCTGGTGCCAACCCGGACCTTCCCCACTTCCTGGTGGAGCCCCGAGGATGTGTACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AY187310 2862 bp mENA linear VR Gallus gallus UNC5-like protein 3 mENA, complete cds. AY187310 AX187310.1 GI:31442350
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larity 61.3%; Pred. No. 2.2e-145;
Conservative 0; Mismatches 961;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ě
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/product="UNC5-like protein
/protein_id="AAO67275.1"
/db_xref="GI:31442351"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organism="Gallus gallus"
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/db_xref="taxon:9031"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gallus gallus (chicken)
                                                                                                                                                                                                                                                                                                                                                                              2786
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Best Local Similarity
Matches 1637; Conserv
   2756
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Pred. No. 3.6e-145;
0; Mismatches 937;
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8727. .8772
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kuramoto, T., Kuwamura, M. and Serikawa, T.
Rat neurological mutations cerebellar vermis defect and hobble are caused by mutations in the netrin-1 receptor gene Unc5h3

Mol. Brain Res. (2003) In press

Z (bases 1 to 9328)

Kuramoto, T. and Serikawa, T.

Direct Submission

Direct Submission

Manimals, Graduate School of Medicine, Kyoto University, Yoshidakonoe-cho, Sakyo-ku, Kyoto 606-8501, Japan

(E-mail:tkuramot@anim.med.kyoto-u.ac.jp,
URL:www.anim.med.kyoto-u.ac.jp,
Fax:81-75-753-4499)
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae;
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GCTTCAGCATCAACTTCAACATCACCAAGGACACAAGGTTTGCTGAGCTGCTGGCTCTGG
                                                                                    rcirccagcigaacigcrcagiarcagagagacccacrgggarrarccarcaigg
                                                                                                                        AGAGTGAAGCGGGGGTCCCAGCCCTGGTGGGCCCCCAGTGCCTTCAAGATCCCCTTCAA
                                                                                                                                                         ATTCAGCAGCACCATCACAACGATAGTTGGGCCCAACGCTTTCAGCATCCCCTCCCAA
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Rattus norvegicus
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KEYWORDS
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TITLE
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AUTHORS
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1044 AGCCGTGA         1159 AGGAGGGA	AGCGTGAGTGCTCTGACCCAGCACCGCAACGGAGGAGGAGGAGTGCCAGGGCACTGAC 1103	A G
1104 CTGGACAC         1219 CTCCAATC	CIGGACACCCGCAACIGIACCAGIGACCTCTGIGIACACAGIGCTTCTGGCCCTGAGGAC 1163 	3 A 8
1164 GTGGCCCT          1279 GTTGCTCT	GIGGCCCTCTATGIGGGCCTCATCGCCGTGGCCGTCTGCTGCTGCTGCTT 1220	à B á
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1569 ACCAGCA 	ACCAGCAACATGACTAT 1586	g qa d
1587 GGGACCT	GGGACCTTCAACTTCCTCGGGGGCCGGCTGATGATCCCTAATACAGGTATCAGCCTCCTC 1646	53 DP 63
1647 ATCCCCC           1810 ATTCCG	ATCCCCCAGATGCCATACCCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCACAAG 1706 	à a
1707 CCGGAAG     1870 AAGAAA	CCGGBABGACGTGAGGTTGCCCCTAGCTGCTGCTGCTGCTGGTGGTCCCATCGTTAGC 1766	Sea
1767 TGTGGAC         1930 TGTGGGC	TGTGGACCCCCTGGCGTCCTGCTCACCCGGCCAGTCATCCTGGCTATGGACCCTGTGGG 1826	
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2546 2666 2826 2786 2366 2586 2486 reracrerercadedaaceracrestaredarrideereredidakeeriderageace 2646 2706 ATTICCAGCCIGGACCCACCCIGIAGGCGGGGIGCCGACTGGCGGACTCTGGCCCAGAAA 2606 2766 CHGGAAGAAHGGGAAGACACAAACCGTAGTGTCCTTGGCAGCAGAAGGTCAGTATTGA 2946 2126 2186 2346 2406 2306 2466 2226 2106 CICCACCIGGACAGCCAICICAGCTICTITGCCTCCAAGCCCCAGCCCCACAGCCCAIGAIC CTTAACCTGGACAGGTACTTGAATTACTTTGCCACCAATCGAGCCGGACTGGCGTAATC 2050 GAGGATCTTGTGGTTG---TTGGAGAGAAAACTTCACAACCCCCTGTTACATTCAGCTG 2307 ACGCAGCGGTACTTGCACTTGCACCTTCGCAGCGTGTCAGCCCCAGCACTGAC 2467 TCTCAAAGAAACCTCCACTGTACCTTCACTCTGGAAAGACTCAGCCTAAACACTAGAG TTCAACATCACCAAGGACACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGG GTCCCAGCCCTGGTGGCCCCCAGTGCCTTCAAGATCCCCTTCCTCATTCGGCAGAAGATA 2707 TGTAGCAGCTGGATGCCCCCCAACAACAAGAGGCCATGACTGGAGGATGCTGGCCCACAAA GTGGCTGGACTGGCCAGCCAGACGCTGGCCTCTTCACAGTGTCGGAGGCTGAGTGCTGA GAGGTGGTGCAGCTGGAGAAGCAGCTGGGGGACAGCTGATCCAGGAGCCACGGGTCCTG 2347 CATTITAAAGGCAGCATCCACAACCTGCGCCTCTCAATTCATGACATCACCCATTCCCTC CTGGCCTGCAAGCTGTGGGTGTGGCAGGTGGAGGCGACGGGCAGAGCTTCAGCATCAAC GAAGITCTACAACTGGAAAGGCAAATGGGAGGACAGCTCCTAGAAGAACCCAAGGCTCTT CACTICAAGGACAGITACCACAACCIGGGCCIAICCAICCACGAIGIGCCCAGCITCCTG GATGCAGAGGCTTGCCATATTCTCACGGAGAACCTCAGTACCTATGCCCTGGTTGGGCAG ACCTCCCTCGAGTACAACATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAG GAGGCCAGTGCCTGCTACGTCTTCACCGAGCAGCTGGGCCGCTTTGCCCTGGTGGGAAG accercadedraderacedeceaadedecercaaderacerrerariadedeceagedecer 2607 2527 2427 2587 2487 2547 2767 2667 2827 2727 2887 2367 2107 2007 2167 2067 2127 2287 2187 1947 5 B 5 B 5 B 5 음 중 음 8 % à Dp के व 8 6 6 6 6 ą ≳

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Total number of hits satisfying chosen parameters:

3373863 seqs, 2124099041 residues

Searched:

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## ALIGNMENTS

RESULT 1

Human; NOVX polypeptide; cardiomyopathy; atherosclerosis; cancer; cell signal processing; metabolic pathway modulation; cancerous tissue; antibody; diabetes; transgenic animal; UNCS-like protein; NOV1; chromosome 13; gene; ds. DNA encoding human UNC5-like protein NOVI. ABK49422 standard; DNA; 2881 BP. (first entry) 15-JUL-2002 ABK49422; **ABK49422** The state of the s

Homo sapiens.

/\*tag= a /product= "Human UNC5-like protein NOV1" Location/Qualifiers 87. .2786 Key

WO200229038-A2

11-APR-2002.

04-OCT-2001; 2001WO-US031377. 04-OCT-2000; 2000US-0237862P.

(CURA-) CURAGEN CORP.

Shimkets RA; Herrmann JL, Rastelli L,

WPI; 2002-340104/37. P-PSDB; AAU79939.

Novel isolated NOVX polypeptide, and encoded polynucleotide, useful for treating cardiomyopathy, artherosclerosis, and cancer.

Claim 8; Page 7-8; 180pp; English.

The present invention relates to a new NOVX polypeptide having a 900 (NOV1), 4349 (NOV2), 940 (NOV3), 798 (NOV4), 865 (NOV5), or 331 (NOV6) residue amino acid sequence, as given in the specification. The novel polypeptide, and its encoding polynucleotide, are used to treat

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cardiomyopathy, atherosclerosis, cancer or a disease related to cell signal processing and metabolic pathway modulation, in a human. Detecting the polypeptide or polynucleotide is useful for identifying cancerous tissue. The antibody can be used to treat diabetes or cancer. The host cells can be used to produce non-human transgenic animals useful in drug screening. The present nucleic acid sequence is that of the human UNCS-like NOVI gene located on chromosome 13. This sequence encodes the human UNCS-like protein NOVI of the invention
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encoding Human protein NOV1
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cell signal processing disorder; metabolic disorder; obesity; infection; anorexia; cancer-associated cachexia; cancer; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorders; dyslipidaemia; pain; asthma; hypertension; osteoporosis; Crohn's disease; multiple sclerosis; argina pectoris; myocardial infarction; ulcer; allergy; benign prostatic hypertrophy; psychosis; neurological disorder; anxiety; schizophrenia; manic depression; dementia; dyskinesia; Huntington's disease; Gilles de la Tourette's syndrome; gene therapy. gene; cardiomyopathy; atherosclerosis;

Homo sapiens.

WO200210216-A2

07-FEB-2002

30-JUL-2001; 2001WO-US024225.

2000US-0222840P. 2000US-0223752P. 28-JUL-2000; 04-AUG-2000; 04-AUG-2000;

04-AUG-2000; 2000US-0223762P. 04-AUG-2000; 2000US-0223769P. 04-AUG-2000; 2000US-0223770P. 14-AUG-2000; 2000US-0225146P. 15-AUG-2000; 2000US-0225392P. 15-AUG-2000; 2000US-0225392P. 

15-AUG-2000; 2000US-0225470P. 16-AUG-2000; 2000US-0225697P. 01-FEB-2001; 2001US-0263662P. 05-APR-2001; 2001US-0281645P.

(CURA-) CURAGEN CORP.

Grosse WM; Smithson G; Casman S, Mezes P, Mishra V, Burgess C, Casman S, , Lepley DM, Gerlach VL, Macdougall JR, Padigaru M, Me Alsobrook JP,

2002-180074/23. P-PSDB; AAU85403 New isolated cytoplasmic, nuclear, membrane bound, or secreted polypeptide, useful for treating cardiomyopathy, atherosclerosis, infections, cancer, neurodegenerative, metabolic, hematopoietic and immune disorders.

Claim 9; Page 9-10; 213pp; English.

The invention relates to an isolated cytoplasmic, nuclear, membrane bound, or secreted polypeptide (NOVX, x= 1-14) their variants or mature form. Also included are the nucleic acids encoding the NOVX proteins, a vector comprising the nucleic acid, a cell comprising the vector, an antiporty and included are the nucleic acid, a cell comprising the vector, an antipox antibody and modulators of NOVX. NOVX, the nucleic acid and the control of the disorder is selected from cardiomypathy.

CC antibody are useful for treathing or preventing a NOVX-associated disorder, where the disorder is selected from cardiomypathy.

CC and metabolic pathway modulation, metabolic disorders, obesity, infectious disease, anorexis, cancer-associated cachexia, cancer, neurodegenerative disorders, Alzheimer's disease, Parkinson's disease, infections disorders, hamatopoletic disorders, and the various of disease, bacterial, fungal, protocoal and viral infections, pain, collimia, asthma, hypertension, uninary retention, osteodystrophy, angina disease, multiple sclerosis, Albright Hereditary Osteodystrophy, angina collication, uninary retention, osteodystrophy, and psychotic and neurological disorders, including anxiety, collimia, manic depression, delinium, dementia, and dyskinesias, collimia, manic depression, delirium, dementia, and dyskinesias, concerterial functions disorders and collicated and curcles and collect and concerted and NOVX protein

BP.

ABK37922 standard; cDNA; 2752

(first entry)

21-MAY-2002

ABK37922;

ABK37922 ID ABK3 XX AC ABK3 XX DT 21-M

RESULT 2

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Netrin binding membrane receptor; receptor; UNC5H-1; gene; ds; human; nootropic; neuroprotective; cytostatic; antiparkinsonian; cerebroprotective; cancer; central nervous system; CNS; stroke; Parkinson's disease; multiple sclerosis; Alzheimer's disease.
                                                                     Human netrin binding membrane receptor UNC5H-1 DNA sequence #1
          ABK52891 standard; DNA; 2697
                                                                                                                                               Ношо
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"Netrin binding membrane receptor UNC5H-1" Location/Qualifiers 1. .2697 /\*tag= a /product= " sapiens

25-APR-2002

WO200233080-A2

15-OCT-2001; 2001WO-EP011891

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This invention relates to the DNA and protein sequences of a novel

CC purified human netrin binding membrane receptor, UNC5H-1. The DNA

Sequence of the invention is useful as a probe for detecting a nucleic

acid encoding the UNC5H-1 protein in a biological sample. The sequences

of the invention are useful to screen for agents which decrease the

activity of the UNC5H-1 protein. The sequences are also useful for

activity of the UNC5H-1 protein. The sequences are also useful for

cscreening agents which regulate (composition containing the protein of

the invention. A pharmaceutical composition containing the protein of

the invention or a reagent that modulates the activity of the UNC5H-1 protein

cmay be useful for treating a UNC5H-1 dysfunction related disease such as

cancer or a central nervous system (CNS) disorders (e.g., parkinson's

disease, multiple sclerosis, stroke and Alzhaimer's disease). Fusion

C proteins comprising the UNC5H-1 protein are useful for generating

creatibodies and for in various assay systems, and the protein can be used

as a bait protein in a two-hybrid assay or three-hybrid assay. The method

cof the invention is useful for detecting a coding sequence encoding the

human netrin binding membrane receptor UNC5H-1 protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87 ATGGCCGTCCGGCCCTGTGGCCAGCGCTCCTGGGCATAGTCCTCGCCGCTTGGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   147 GGCGGCTCGGGTGCCCAGCAGAGTGCCACCGTGGCCAACCCAGTGCCTGGTGCCAACCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6
                                                                                                                                                                                                                Novel human netrin binding membrane receptor polypeptide and polynucleotides for identifying modulating agents useful in the diseases e.g. Parkinson's disease, multiple sclerosis, stroke,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 6; Length 2697;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2697 BP; 503 A; 906 C; 807 G; 481 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25; Indels
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                                                                                                                                                                                                                                                                                                                           Claim 1; Fig 1; 94pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90.8%;
                      16-OCT-2000; 2000US-0240061P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 2669; Conservative
                                                                                                                                                   WPI; 2002-463314/49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                         P-PSDB; AAU97899.
                                                               (FARB ) BAYER AG
                                                                                                                                                                                                                                                                                    Alzheimer's
                                                                                                            Koehler RH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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180 326 240 386

GTGCTGCTTGTGTGCAAGGCCGTGCCCGCCACGAGATCTTCTTCAAGTGCAACGGGGAG GTGCTTGTTGTTGTGTGCAAGGCCGTGCCCGCCACGAATCTTCTTCAAGTGCAACGGGGAG TGGGTGCGCCAGGTGGACCACGTGATCGAGCGCAGCACAGAGCGGGAGCAGTGGTGAGCCG

181

267

 $\delta$ g  $\delta$ g à 셤

241

387

TGGGTGCCCAGGTGGACCACGTGATCGAGCGCAGCACAGAGCAGGAGCAGTGCCC 300

ACCATGGAGGTCCGCATTAATGTCTCAAGGCAGCAGGTCGAGAAGGTGTTCGGGCTGGAG

ACCATGGAGGTCCGCATTAATGTCTCTAAGGCAGGTCGAGAAGGTGTTCGGGCTGGAG GAATACTGGTGCCAGTGCGTGGCATGGAGCTCCTCGGGCACCACCAAGAGTCAGAAGGCC GAATACTGGTGCCAGTGCGTGGCATGGAGCTCCTCGGGCACCACCAAGAGTCAGAAGGCC

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TACATCCGCATAGCCAGATTGCGCAAGAACTTCGAGCAGGAGCCGCTGGCCAAGGAGGTG 

1544 CTCATCCCCCCAATACCCATACCCCAAGGAAAACTATACAACTCCCCCAAGGCTCCCAACTCCTCCCAACCCTCCCCAACCCTCCCCAACCCTCCCCAACCCTCCCCCAACCCTCCCCCC
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human; antiinflammatory; cytostatic; immunosuppressive; antiviral;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This invention relates to twelve human receptors cDNA sequences referred to as REPTR-1 to REPTR-12), and the proteins encoded thereby. The proteins of the invention may have antiinflammatory, cytostatic, immunosuppressive, antiiviral, anti-HIV, antiarthritic, muscular active general, anticonvulsant, nootropic, neuroprotective, antiallergic activities. The sequences of the invention may be used to produce REPTR agonists or antagonists, and the protein sequences may be used to raise
2635 GCAGTGGCTGGACTGGCCAGCCAGCCTGGTGCTTCACAGTGTCGCAGGCTGATGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             developmental disorder; Duchenne muscular dystrophy; gene;
Becker muscular dystrophy; neurological disorder; epilepsy;
Alzheimer's disease; Huntington's disease; reproductive disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                anti-HIV; antiarthritic; anticonvulsant; noctropic; neuroprotective; antiallergic; antibody; immunogen; endometriosis; carcinocarinal disorder; gastritics; oscophageal carcinoma; crohn's disease; irritable bowel syndrome; ulcerative colitis; endocrine disorder; hypothalamus disorder; Kallman's disease; autoimmune disease; inflammatory disease; inflettlity; receptor; autoinmune deficiency syndrome; ALDS; rheumatoid arthritis; allosteentritis; diabetes mellitus; multiple sclerosis; systemic lupus erythematosus; cell proliferative disorder; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Twelve human receptors (referred to as REPTR-1 to REPTR-12), useful the diagnosis, treatment and prevention of gastrointestinal (e.g. gastritis), autoimmune/inflammatory (e.g. osteoarthritis) and cell proliferative (e.g. cancer)disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Griffin JA, Kallick DA, Tribouley CM, Yue H, Nguyen DB, Lal P, Policky JL, Azimzai Y, Lu DAM, Graul R, Yao MG, Hafalia AJA, Baughn MR, Bandman O, Patterson C, Yang J, Gandhi AR, Warren BA, Ding L, Sanjanwala MS, Duggan BM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product= "REPTR1 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 57; Page 142-143; 157pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ocation/Qualifiers
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25-AUG-2000; 2000US-0228045P.
12-DEC-2000; 2000US-0255104P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REPTR 1 cDNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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/*tag= a
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                                                                                                                                                                                                                                                                                                                                             ABK15169 standard;
                                                                                                          TGA 2786
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anti-REPTR antibodies. These molecules and the REPTR polynucleotides and polypeptides of the invention are useful in the diagnosis, treatment and prevention of gastrointestinal (e.g. gastritis, oesophageal carcinoma, crohn's disease, irritable bowel syndrome, ulcerative colitis), endocrine (e.g. hypothalamus disorder, Kallman's disease), autoimmune/ inflammatory (e.g. arquired immune deficiency syndrome (AIDS), rheumatoid arthritis, allargies, osteoarthritis, diabetes mellitus, multiple sclerosis, systemic lupus erythematosus), cell proliferative (e.g. cancer), developmental (e.g. Duchenne and Becker muscular dystrophy), neurological (e.g. epilepsy, Albeimer's disease, Huntington's disease) and reproductive (e.g. infertility, endometriosis) disorders. Numerous other examples of each disorder are given in the specification. The present sequence represents the human REPTRI CDNA sequence of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, petide therapy. The polypeptides have various cytokine-like activities, activity, tissue growth factor activity, immunomodulatory activity and activity, issue growth factor activity, immunomodulatory activity and activity, insue prowth factor activity, immunomodulatory activity and treatment of cancer, leuksemia, nervous system disorders, arthritis and inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acids encoding polypeptides with cytokine-like activities, useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        192
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Wang
Human, cytokine, cell proliferation, cell differentiation, gene the vaccine, peptide therapy, stem cell growth factor, haematopoiesis, tissue growth factor, immunomodulatory, cancer, leukaemia, nervous system disorder, arthritis, inflammation, ss.
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Chen R,
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Yang D, Wang J, Zhang J,
Wejhrman T, Goodrich R;
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Pred. No. 0;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                       03-FEB-2000; 2000US-00496914.
27-APR-2000; 2000US-00560875.
20-JUN-2000; 2000US-00598075.
19-JUL-2000; 2000US-00650325.
01-SEP-2000; 2000US-00654936.
15-SEP-2000; 2000US-00663561.
20-OCT-2000; 2000US-00693325.
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Wejhrman T,
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Matches 2565; Conservative
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, Yang Y,
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                                                                                                                                     Homo sapiens
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QY         2458 AGCTGCTGGCTCTGGAGAGTGAAGCGGGGGTCCCTGGTGGCCCCAGTGCCTTCA         2517           Db         2579 AGCTGCTTGGAGAGTGAAGCGGGGGTCCCAGCCCTGGTGGCCTCTAGGCGTTCA         2638           Db         2518 AGCTCCTTTCGGCAGAGATTTTCCAGCCTGGACCCAGTGCTTTAGGCGGG         2577           Db         2538 AGTCCCTTTCTTCGGCAGAAGATTTTCCAGCCTGGACCCACCTGTAGGCGGG         2578           QY         2578 GTGCCGACTGGACGGACTCTGGCCAGAAGTTTCCAGCCTGGACCCACCTGTAGGCGGG         2698           QY         2599 GTGCCGACTGGCGGACTCTGGCCCAGAAGTTCACCTGGACCACTCTCAGCTTTTTG         2758           QY         2698 ACGCCAAGCCCAGCCCATGATCCTCAACCTGTGGGCGCACTTCTTTG         2758           QY         2698 ACGCCAAGCCCAGCCCAGAAACTCCACTCACCTGGGCGCACTTCTTTG         2759           QY         2698 ACGCCAAGCCCAGCCATGATCCTCAACCTGTGGGCGCACTTCTCCCA         2818           QY         2759 CTTCCAAGCCCAGCCCACGCCAGACTGGTCGACTGGGCCAGCCA	OLL S	XX 19-FEB-1998; 98WO-US003143.  XX 19-FEB-1997; 97US-00808982.  XX 19-FEB-1997; 97US-00808982.  XX 19-FEB-1997; 97US-00808982.  XX X
1487 CCAGCAAAGCAGACACCCCATCTGCTCAGCACCGGACCTCAGCACCACCAC 1546  1378 CCACCTACCAGGGCAGTCTCTGTCCCGGCAGGATGGGCCCCAGGTCCAGCTCA 1437		CTACT 2218  3GGGG 2178  GGGCC 2217  GGGCC 2217  GGGCC 2338  GCAGG 2277  CCAGG 2277  CCAGG 2277  CCAGG 2277  CCAGG 2298  GGTGC 2458  GGTGG 2457  TGCTG 2457  TGCTG 2457

AAVS2941) and unc5h-2 (see AAVS2943) cDNAs are also claimed. Vertebrate UNC-5 proteins may be produced recombinantly from transfected host cells by utilising these vertebrate UNC-5 nucleic acids. The invention also provides unc-5 hybridisation probes and primers, vertebrate UNC-5 specific binding agents such as specific antibodies, and methods of making and using the subject compositions in diagnosis (e.g. genetic hybridisation screens for vertebrate unc-5 transcripts), therapy (e.g. gene therapy to modulate vertebrate unc-5 gene expression) and in the biopharmaceutical industry (e.g. as immunogens, reagents for modulating pharmacological agents for screening chemical libraries for lead pharmacological agents, etc.). (Updated on 25-MAR-2003 to correct PI 8X33333333333X8

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146 CGCGGCTCGGGTGCCCAGCAGAGTGCCACCGTGGCCAACCCAGTGCCTGGTGCCAACCCG 206 266 120 420 326 TGGGTGCGCCAGGTGGACCACGTGATCGAGCGCAGCACAGACGGAGCAGTGGTGAGCCG 386 446 506 566 480 626 540 686 900 746 099 806 866 926 9 780 ATGGCCGTCCGGCCCGGCCTGTGGCCAGCGCTCCTGGGCATAGTCCTCGCCGCTTGGCTC GACCTGCTTCCCCCACTTCCTGGTGGAGCCCGAGGATGTGTACATCGTCAAGAACAAGCCA GTGCTGCTTGTGTGCAAGGCCGTGCCCGCCACAGATCTTCTTCAAGTGCAACGGGAG Ardecertedeceredecereredecererederecredecaracteredeceredecredecer ACCATGGAGGTCCGCATTAATGTCTCAAGGCAGCAGGTCGAGAAGGTGTTCGGGCTGGAG GAATACTGGTGCCAGGCATGGAGCTCCTCGGGCACCACCAAGAGTCAGAAGGCC TACATCCGCATAGCCAGATTGCGCAAGAACTTCGAGCAGGAGCCGCTGGCCAAGGAGGTG TACATCCGGATTGCCTATTTGCGCAAGACTTTGAGCAGGAGCCACTGGCCAAGGAAGTG TCCCTGGAGCAGGCATCGTGCTGCCTGCCGTCCAGCGGAGGGCATCCCTCCAGCCGAG TCACTGGAGCAAGGCATTGTACTACCTTGTCGCCCCCCAGAAGGAATCCCCCCAGCTGAG GIGGAGIGGCICCGGAACGAGGACCIGGIGGACCCGITCGACCCCCAAIGIAIACAIC ACGCGGGAGCACCAGCTGGTGCGACAGGCCCGCCTTGCTGACACGGCCAACTACACC TGCGTGGCCAAGAACATCGTGGCACGTCGCCGCAGCGCCTCCGCTGCTGTCATCGTCTAC GTGAACGGTGGTGGTCGACCGACCGAGTCCGTCTGCAGCGCGCAAGCTGTGGGCGC GGCTGGCAGAAACGGAGCCGGAGCTGCAACCCGGCGCTCTCAACGGGGGGCGCTTTC Length 3014; 11; Sequence 3014 BP; 596 A; 977 C; 849 G; 592 T; 0 U; 0 Other; Indels DB 2; 312; Score 2235.8; Pred. No. 0; 0; Mismatches 77.6%; 88.5%; Conservative Best Local Similarity Matches 2474; Conser Match 147 61 207 121 267 181 327 241 387 301 447 361 507 747 421 567 481 627 541 687 601 199 807 721 867 field.)

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qq	898 AGCTGGAGTTCGTGGAGTAAGTGGTCAGCCTGTGGGCTTGACTGCACCACTGGCGGAGC 957
δ	1047 CGTGAGTGCTCTGACCCAGCACCCGCAACGGAGGGGGGGG
qq	958 CGCGAGTGCTCTGACCCAGCACCCCGCAATGGAGGTGAGGAGTGTCGGGGGTGCTGACCTG 1017
ΟŻ	1107 GACACCCCCAACTGTACCAGTGACCTCTGTGTACACAGTGCTTCTGGCCCTGAGGACGTG 1166
QD	1018 GACACCGGCAACTGTACCAGTGACCTCGCTGCACACGCTTCTTGCCCCGAGGACGTG 1077
ò	1167 GCCTCTAIGIGGGCCTCAICGCCGIGGGCGTCCTGCTGCTGCTTGTCCTC 1226
Dp	1078 GCTCTCTACATCGGCCTTGTCGTGTGGCTGTGCCCTCTTCTTGCTGCTGTGGCCCTT 1137
δλ	1227 ATCCTCGTTTATTGCCGGAAGAAGGGGCTGGACTCAGATGTGGCTGACTCGTCCATT 1286
qq	1138 GGACTCATTTACTGTCGCAAGAAGGAACGGCTCGGATGTGGCCCGACTCGTCCATC 1197
δλ	1287 CTCACCTCAGGCTTCCAGCCCGTCAAGCCCAGCAAAGCAGACAAACCCCCATCTG 1346
qq	1198 CTCACCTCGGGCTTCCAGCCTGTCAGCATCAAGCCCAGCAAAGCAGACAACCCCCACCTG 1257
ζ	1347 CTCACCATCCAGCCGGACCTCAGCACCACCACCAGGGCAGTCTCTGTCCC 1403
qu	1258 CTCACCATCCAGCCAGACCTCAGCACCACCACCACCACCACCAGGGGCAGTCTATGTTCG 1317
ò	1404 CGGCAGGATGGGCCCCAAGTTCCAGCTCAACCAATGGGCACTGCTCAGCCCCTG 1463
qq	1318 AGGCAGGATGGACCCAGCCCCAAGTTCCAGCTCTCTAATGGTCACCTGGTCAGCCCACTG 1377
δ	1464 GGTGGCGCCGCCACACACACACACACACTCCCACCTCTGAGGCCGAGGATTCGTC 1523
ΩÞ	1378 GGGAGTGGCCCATACGTTGCACCACAGCTCACCCACTCTGAGGCTGAGGACTTCGTC 1437
λŏ	1524 TCCGGCTGTCCACCAGAACTACTTCCGCTCCCTGCCCCGAGGCACCAGCAACATGACC 1583
qq	1438 TCCGGCCTCTCCACCCAAACTACTTTCGTTCCTGCCCCGGGGCACCAGCAACATGGCC 1497
ò	1584 TATGGGACCTTCAACTTCCTCGGGGGCCGGCTGATGATCCCTAATACAGGTATCAGCCTC 1643
qa	1498 TACGGGACCTTCAACTTCCTCGGGGGCCGGCTGATGGTCCTAATACGGGGATCAGCCTC 1557
ζ	1644 CTCATCCCCCCAGAIGCCATACCCCGAGGAAGATCTATGAGATCTACCTCACGCTGCAC 1703
đ	1558 CTCATACCCCCGGATGCCATCCCCCGAGGAAAGATCTACGAGATCTACCATCACACACA
ò	1704 AAGCCGGAAGACGTGAGGTTGCCCCTAGCTGGCTGTCAGACCCTGCTGAGTCCCATCGTT 1763
qq	1618 AAGCCAGAAGACGTGAGGTTGCCCCTAGCTGGCTGTCAGACCCTGCTGAGTCCAGTCGTT 1677
ò	1764 AGCTGTGGACCCCTGGCGTCTGCTCACCGGCCAGTCATGGACTATGGACCACTGT 1823
qq	1678 AGTIGITGGCCCCCCAGAGICCTCACCCGGCCAGTCATCCTTGCAATGGACCACTGT 1737
'n	24 GGGGAGCCCAGCCGAGAGCTGGAGCCTCAAAAAGCAGTCGTGCGAGGGCAGC
qq	1738 GGAGAGCCCAGCCTGACAGCTGGAGTCTGCGCCTCAAAAAGCAGTCCTGCGAGGGCAGT 1797
λo ·	1884 TGGGAGCAGGATGTGCTGCACCTGCGCGGGCGCCCTCCCACCTCTACTACTGCCAG 1943
අු	1798 TGGGAGGATGTGCTGCACCTTGGTGAGGAGTCACCTTCCCACCTCTACTACTGCCAG 1854
<i>장</i> 원	1944 CTGGAGGCCAGTGCTACGTCTTCACCGAGCAGCTGGGCCGCTTTGCCCTGGTGGG 2003
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local cerebral glucose utilisation, phosphodiesterase 1-alpha, UNCSH1, calcium-independent alpha-latrotoxin receptor; CIRL; trkE; synapsin 1A; epithelial discoidin domain receptor 1; synapsin 1B; neuroleptic; ss;

tůmour necrosis factor alpha; TNF-alpha; rat

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Location/Qualifiers 1. .2697 /\*tag= a

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Novel chronic animal model of schizophrenia, useful for identifying antipsychotic drugs and genes that are associated with schizophrenia.

English

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Claim 1; Fig

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Pratt

В,

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Ohashi

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Cochran S, Paterson (WELF-) WELFIDE CORP

2002-010813/01.

P-PSDB; AAU10543

31-MAR-2000; 2000GB-0007880. 26-MAY-2000; 2000GB-00012768. 02-APR-2001; 2001WO-GB001486.

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The invention relates to YSG polynucleotide fragments for use in diagnosing and/or developing treatments for schizophrenia using chronic diagnosing and/or developing treatments for schizophrenia using chronic animal models. The polynepitoles and their encoded polypeptides are sequences can also be used for testing candidate compounds for any effect sequences can also be used for testing candidate compounds for any effect on the polypeptides. Anti-schizophrenic effects of a compound can be determined by measuring local cerebral glucose utilisation (LCGU) or comparing its expression level with that of a control group. The sequences are useful in the identification of genes associated with schizophrenic states and in the development of an antibody. The sequences of the invention include phosphodiesterase 1-alpha, calcium-independent alpha-latrotoxin receptors (CTEL)-1,2&3, epithelial discoidin domain receptor (TEKE), netrin receptor (WINCSHI), synapsins lA and AB and tumour necrosis factor (TMF) alpha. This sequence represents rat netrin receptor UNCSHI (YSG7) DNA
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Pred. No. 0;
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88.9%;
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Best Local Similarity
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Matches 2403;
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2697

CDNA;

AAS16843 standard;

RESULT

AAS16843

AAS16843 ID AAS1 XX AAS1 XX AAS1 XX I4-F XY I4-F XX XX

Rat

1318   AGGCAGGACCCAAGCTCCAAGCTCCTAATGGTCACCTGCTCAGCCCACTG   1377   1464   GGTGGCGCCACACACCCCACCACCTCTCAATGGTCACCTCCAGGCCCACGAGGACTTCGTC   1523   1378   GGGGGCGCCCCATACCACACCACACCCCCCCCCCCACGAGGCTTCGTC   1437   1524   TCCCGCCTCTCCACGCACCACACACACACACACACACACA	1 1 2 1 5 1 5 1 5 1 5 1 5 1 5 1 5 1 5 1			1855 CTGGAGGCCGGGGCCTGCTATGTCTTCACGGAĠCAĠCĠCGTTTGCCCTĠGTAGĠA 1914 2004 GAGGCCCTCAGCGTGGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCGGGTGGCC 2063	2064 TGCACCTCCGAGTACAACATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTC 2123				2335 AACTTCAACATCACAACACAAGAGTTTGCTGAGCTGCTGGAGGTGAAGGG 2483 2335 AACTTCAACATCACTAAGACACAAGGTTTGCTGAATTGTTGGCGAGAGTGAAGGG 2394 2484 GGGGTCCCAGCCCTGGTGGGCCCCAGTGCCTTTGAATTCTTCTCTCATTCGGCAGAGTCAAGGG 2543 [
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us-09-970-944-1.rng

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Cc caenorhabditis elegans unc-5. unc5h-1 and unc5h-2 (see AAV52943) cDNAs were isolated from an embryonic brain cDNA library. The predicted comparients (see AAW78891) show similarity with UNC-5. They are predicted to be involved in cell migration and axon guidance, and are coharcterised as receptor proteins for netrins. Gene expression is conserved in regions where differentiating neurons are undergoing axogogenesis. Rat unc5h-1 (see AAV52940) and unc5h-2 (see AAV52941) cDNAs are also claimed. Vertebrate UNC-5 proteins may be produced recombinantly from transfected host cells by utilising these vertebrate UNC-5 nucleic acids. The invention also provides unc-5 hybridisation probes and caids. The invention also provides unc-5 hybridisation probes and cids. The invention also provides unc-5 hybridisation probes and cidsonosis (e.g. genetic hybridisation screens for vertebrate unc-5 antibodies, and methods of maxing and using the subject compositions in cidagnosis (e.g. genetic hybridisation screens for vertebrate unc-5 cranscripts), therapy (e.g. gene therapy to modulate vertebrate unc-5 cranscripts), therapy (e.g. gene therapy to modulate vertebrate unc-5 cranscripts), therapy (e.g. gene therapy to modulate vertebrate unc-5 inmunospens, reagents for modulating cell guidance, reagents for screening chemical libraries for lead pharmacological agents, reagents for screening chemical libraries for lead pharmacological agents.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1787;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 1570.4; DB 2,
Pred. No. 5.6e-280;
0; Mismatches 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54.5%;
96.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 96.9<sup>3</sup>
Matches 1721; Conservative
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1718 GAGGTTGCCCCTAGCTGGCTGTCAGACCCTGCTGAGTCCCATCGTTAGCTGTGGACCCCC 1777 TGCCATACCCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCACAGCCGGAAGACGT 246 The present invention describes 3 variants of human unc-5C cDNAs (unc-5Cb, unc-5Cc and unc-5C8) which correspond to alternatively spliced unc-5Cb, unc-5Cc and unc-5HS1 cDNA which shares homology with the Ratus norvegicus unc-5HS1 cDNA. Also described are assays based on protein-interactions between the unc-5 protein and a variety of different interacting proteins. The unc-5C variant cDNAs and unc-5HS1 cDNA are useful in methods for identifying compounds which reduce or inhibit the lethal phenotype associated with the expression of the unc-5 death domain in yeast. They are also useful in yeast two hybrid experiments for identifying unknown human cDNAs which encode proteins that interact with the human unc-5C protein. AAC90914 to AAC90971 and AABS0646 to AABS0693 represent sequences used in the exemplification of the present invention with 1478 CACACTGCACCACAGCTCTCCCACCTCTGAGGCCGAGGAGTTCGTCTCCCGCCTCTCCAC CACACTGCACCACACCTCCCCACCTCTGAGGCCGAGGAGTTCGTCTCCCGCCTCTCCAC TGCCATACCCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCACAAGCCGGAAGACGT 1538 CCAGAACTACTTCCGCTCCCTGCCCCGAGGCACCAGCAACATGACCTATGGGACCTTCAA CTICCTCGGGGGCCGGCTGATGATCCCTAATACAGGTATCAGCCTCCTCATCCCCCCAGA variant; nematode worm; Gaps Three variants of human unc-5C cDNAs (unc-5Cb, unc-5Cc and unc-5C8) human unc-5HS1 cDNA, useful in yeast two hybrid experiments for identifying unknown human cDNAs which encode proteins that interact 3; Sequence 9700 BP; 2604 A; 2193 C; 2236 G; 2666 T; 0 U; 1 Other; Length 9700; 3; Indels Ъ; Verwaerde 44.8%; Score 1291.2; DB 4; 99.5%; Pred. No. 1.8e-228; ive 0; Mismatches 3; Plasmid pGC1037 nucleotide sequence SEQ ID NO:91 Human, Caenorhabditis elegans; UNC-5; splice protein-protein interaction; identification; Bogaert T, Example 4; Page 228-230; 246pp; English. BP. AAC90958 standard; cDNA; 9700 Roelens I, 02-JUN-2000; 2000WO-EP005108 99GB-00012755 the human unc-5C protein. Best Local Similarity 99.5 Matches 1306, Conservative WPI; 2001-016508/02. Ŋ. Van Criekinge W, WO200073328-A2 (DEVG-) DEVGEN 01-JUN-1999; 19-MAR-2001 07-DEC-2000 AAC90958 <u>\_</u> 1658 187 1598 Query Match 67 127 AAC90958 RESULT d à d ð à qq  $\overset{\circ}{\circ}$ qq

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AAM25963. The proteins can have activities based on the tissues and cells they are expressed in, such as: antiinflammatory; antirheumatic; they are expressed in, such as: antiinflammatory; antirheumatic; antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant; central nervous system; virucide; antibacterial; endocrine; cardiant; central nervous system; virucide; antibacterial; endocrine; cardiavascular; antianaemic; antiagregant; hamostaid; vulnerary; antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic; antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic; antiparkinsonian; and immunostimulant. The proteins and polynucleotides concoding them can be used in gene therapy, antisense therapy and vaccine production. The proteins and polynucleotides are useful for screening for production. The proteins and polynucleotides are useful for screening for agonists or antagonists of a protein and for the treatment and diagnosis of disorders associated with the activity of a protein e.g. inflammation, rhemmatoid arbritis, septic shock, pancreatitis, cardiac dysfunction, conference, nulcimmunity, genetic diseases, hammatopoietic disorders, infections, autoimmunity, genetic diseases, hammatopoietic disorders, canaemia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers, chinitis, asthma, diabetes, cancer, multiple sclerosis, depression, chinitis, asthma, diabetes, cancer, multiple sclerosis, depression, contemporative and contents and disease, parkinson's disease, neurodegenerative and contents and 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          thrombocytopaenia; osteoporosis; severe combined immunodeficiency;
allergic rhinitis; diabetes; multiple sclerosis; depression;
Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;
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                                                                                                                                                                                                                                            Human; cancer; ulcer; HIV infection; human immunodeficiency virus;
                                                                                                                                                                                         Human protein encoding cDNA sequence SEQ ID NO:365.
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                         AAH99530 standard; cDNA; 1321 BP
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21-JAN-2000; 2000US-00488725.
25-APR-2000; 2000US-00552317.
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The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders
                                                                                                                                        1138 CCTGGACAGCCATCTCAGCTTCTTTGCCTCCAAGCCCAGCCCAGGCCATGATCCTCAA
                         AGCCCTGGTGGCCCCAGTGCCTTCAAGATCCCCTTCCTCATTCGGCAGAAGATAATTTC
                                                     CAGCCTGGACCCACCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAACTCCA
                                                                                    1078 CAGCCIGGACCCACCCIGIAGGCGGGGGGCGACTGGCGGGACTCCGA
                                                                                                                    CCTGGACAGCCATCTCAGCTTCTTTGCCTCCAAGCCCCACACACCATGATCCTCAA
                                                                                                                                                                                  T-GGACTGGGCCAGCCAGACGCTGGCCTC-TTCACAGTG-TCGGAGGCTGAGTGCTGAGG
        ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; chromosome mapping; gene mapping; gene therapy; forensic; supplement; medical imaging; diagnostic; genetic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA encoding novel human diagnostic protein #11542.
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                                     Gaps
                                 10;
     Length 1321;
                                 Indels
   4,
 Score 1193.6; DB 4;
Pred. No. 1.4e-210;
0; Mismatches 19;
 41.4%;
97.8%;
             Best Local Similarity 97.8
Matches 1295; Conservative
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polypeptide and polynucleotide sequences have applications in diagnostics, forenatics, gene mapping, identification of mutations in tesponsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                   Length 3646;
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Pred. No. 2.1e-159;
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Sequence 2860 BP; 555 A; 950 C; 860 G; 495 T; 0 U; 0 Other;
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                                                                                    Pred. No. 1.9e-154;
0; Mismatches 960; Indels 102;
30.9%;
                                                                                                                                                     Matches 1637; Conservative
                                                                          Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDNA; 2860
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ABT06279 ABT06279

ABT06279
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AC ABT0
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DX
XX
DX
CX
XX
DB Hume
XX
KW Hume
KW St01
KW St

7;

Gaps

Length 2860;

; DB 6; L 1.9e-154;

Score 889;

243

303

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            several novel human proteins, designated NOVX. These can be used in the treatment of, amongst others, cancers, autoimmune diseases, infections, inflammatory diseases, storage disorders, muscle disorders, neurodegenerative diseases and developmental defects. The present
antiinfertility; antimanic; antiuloer; cerebroprotective; anticonvulsant; tranquilizer; analgesic; gene; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention provides the protein and coding sequences of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Grosse WM, Alsobrook JP, Lepley DM, Rieger D, Bw
Spytek KA, Boldog FL, Li L, Padigaru M, Mishra V
M, Shenoy S, Rastelli L, Tchernev VT, Vernet CAM,
M, Malyankar UM, Guo X, Miller CE, Gangolli EA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  designated NOVX, useful for treating
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Lepley DM, Rieger D,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 9; Page 11; 353pp; English.
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25-JAN-2001; 2001US-0264180P.
20-AUG-2001; 2001US-0313656P.
05-OCT-2001; 2001US-0327456P.
28-NOV-2001; 2001US-00327456F.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CURA-) CURAGEN CORP.
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Patturajan M,
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30-NOV-2000;
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Gerlach V,
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CCCAGAACTACTTCC		δ
CTGG	54	<b>₹</b> 48
GCACCACGGGCTCTGGGGCCAGG	1485	8 8
	نو:	ΟŻ
	1425	qq
TCACCAATGGGCACCTGCTCAGCCCC	1435	δλ
GCGCCGCATCTACCGCGGACCCGTGTATGCCCTG	1365	Db
CCACCACCTACCAGGGCAGTCTCTGTCCCCGGCAG	1375	δλ
cgccaaggcccagtaaccccccccc	1305	qq
1 CCAGCAAAGCAGACAACCCCATCTGCTCJ	1321	δy
CAGACATCACTGATCTGCTGCCTGACTGGT	1245	ΩD
CAGATGTGGCTGACTCGTCCATTCTCACCTCAC	1264	δy
	1185	qu
regrecrecrecrecrectrercarecregation.	1204	QY
TGGAGGCCTCAGGGGATGCGGCGCTGTATGCGGGG	1125	ΩÞ
GTGCTTCTGGCCCTGAGGACGTGGCCCTCTATGTG	1144	δλ
GTGACTGCAGCGGGGCTGCTCGACTCTAAGAAC	1065	Ωp
AGGAGTGCCAGGGCACTGACCTGGACACCCGCAACT	1084	δλ
CTGAGTGTGCCCACTGGCGTAGCCGCGAGTGCATG	1005	qa
TGGACTGCACCGCGCGGAGCCGTGAGTGCTCTC	1024	δλ
5 CCACCATCTGCCAGTGGGGCGTGGACGGAGT	945	QQ
CTCTGCTTGTCTCTGTGGACGGCAGCTGGAGCCCG	964	δλ
crccacrcaacgggggccrrcrgcgagggccag	888	Ob
CGCCTCTCAACGGGGGCGCTTTCTGTGAGGGGCAG4	904	δλ
CCTGCTCCAACGCTGTGGCCGAGGCTGGCAGAAGG	828	ΩÞ
TCTGCAGCGCCAGGCTGTGGGCGCGGCGGCTGGCAGAAAC	844	ò
ccactdccaccgrcatcGrcracgrdaargGcGGC	768	qq
CCTCCGCTGCTGTCATCGTCTACGTGAACGGTGGGT	784	δχ
	708	qq
AACTACACCTGCGTGGC	724	ò
	648	qu
CCCTGGACCCCAATGTATACATCACGCGGGAGCACA	664	δy
CGGAGGGGGCCTGTGCCGAGGTGGAATGGCTCCA	588	qu
CGGAGGCATCCCTCCAGCCGAGGTGGAGTGGCTCC	604	δλ
AGGAGCCTCTGGCCAAGGAGGTGCCCCTGGACCATG	528	QQ
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2607 2310 2667 2190 2261 2487 2681 2010 2201 1664 2081 TITCCAGCCTGGACCCACCCTGTAGGCGGGGTGCCGACTGGCCGGACTCTGGCCCAGAAAC gcaacagccradargccccccaacrcacgggcaargacrggcggargrragcacagaagc TCCACCTGGACAGCCATCTCAGCTTCTTTGCCTCCAGCCCAGCCCAGGCATGATCC --daggiggigarcerggargagagacergaacacecrgeracracrageragg crehechadabacacenechedenecenedacaenenenerereteeeerideeaeaeard TCCCAGCCCTGGTGGCCCCCAGTGCCTTCAAGATCCCCTTCCTCATTCGGCAGAAGATAA AAAGTACCCTGCCGCTTTCAGAAGGGACCCAGACAGTATTGAGCCCCTCGGTGACCTGTG GACCCCTGGCGTCCTGCTCACCCGGCCAGTCATCCTGGCTATGGACCACTGTGGGGAGC ccadedectercacarecradaceaderedececeracererreadededederecr 2082 ATTCCGGCTCAGCAGAGCGGCTCCAGCTGGCGTCTTCGCCCCCGCCCTCTGCACCT GGAGCAAGCTGCCCAAATACCAGGAGATCCCCTTCTATCACATTTGGAGTGGCAGCC AGOGGIACTIGCACTGCACCTTCACCCTGGAGCGTGTCAGCCCCAGCACTAGTGACCTGG adaadgecerecaerdedeerrredeerdadadgedeacadgerregeeredadagerea ACATCACCAAG---GACACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGG AAGACGTGGCTTGCCCCTAGCTGGCTGTCAGACCCTGCTGAGTCCCATCGTTAGCTGTG CCAGCCCTGACAGCTGGAGCCTGAAAAAGCAGTCGTGCGAGGGCAGCTGGGAAGC AGGATGTGCTGCACCTGGGCGAGGAGGCGCCTCCCCACCTCTACTACTGCCAGCTGGAGG TCAGCGTGGCGCCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCCGGTGGCCTGCACCT CCCTCGAGTACAACATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAGG TGGTGCAGCTGGAGAAGCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCCTGCACT TCAAGGACAGTTACCACAACCTGCGCCTATCCATCCACGATGTGCCCAGGCTCCCTGTGGA AGAGTAAGCTCCTTGTCAGCTACCAGGAGATCCCCTTTTATCACATCTGGAATGGCACGC CCTGCAAGCTGTGGGTGGCCAGGTGGAGGGCGACGAGGCCAGAGCTTCAGCATCAACTTCA cerecaasarcrecerecesaaresaasesesasesecaaarrecaserecaraa CCTTCAACTTCCTCGGGGGCCGGCTGATGCCCTAATACAGGTATCAGCCTCCTCATCC cerrraserracerrasarasasas en caraceracas es es es es estas es en estas en en estas en en estas en en estas en en estas en CCCCAGATGCCATACCCCGAGGAAGATCTATGAGATCTACCTCACGCTGCACAAGCCGG TCAGTGCCGTGACTGGATCTTTCAGCTCAGAGCCCAGGGCCACAGGGCCACTGGGAG-CCAGTGCCTGCTACGTCTTCACCGAGCAGCTGGGCCGCTTTGCCCTGGTGGGAGAGGCCC 2202 2371 2442 2502 2548 2191 2262 2251 2322 2311 2382 2431 2488 2562 2622 2608 1845 1831 1951 2022 2011 2131 1665 1651 1725 1711 1785 1771 1905 1891 1964 1591 1605 D<sub>P</sub> 장염 9 de 9 de 2 8 à 8 6 6 6 8 8 8 g & 9 9 9 6 6 6 6 6 6 원 장 원 8 6 6 1476 1604 1083 1143 1124 1203 1184 1263 1244 1320 1304 1374 1364 1434 1424 1460 GGCACCAGCAACATGACCTATGGGA 1590 1004 recadecaagreerececererese 1023 GCGCCCCACCCCAGAACGGAGGCC 1064 587 783 843 827 903 887 963 944 603 663 647 723 707 167 TGTACCAGTGACCTCTGTGTACACA rdcacagardescrerecarecae GGCTTCCAGCCCGTCAGCATCAAGC GATGGGCCCAGCCCCAAGTTCCAGC CAGGACTCCACCGACAAAATCCCCA CTTAAGGTCAAGGTCTACAGCTCCA GAGGAGTICGTCTCCGGCCTCTCCA cactrocrecacerececaececa GACCCAGCACCCCGCAACGGAGGGG Crceregrecenterregregre TGCCGGAAGAAGGAGGGGCTGGACT GGTTTCCACCCCGTCAACTTTAAGA ACCATCCAGCCGGACCTCAGCACCA rergrecercercadedadadadadad ------GCTGACCTGCTGGGGGTCTTGCCGC GGCCTCATCGCCGTGGCCGTCTGCC Céccecaacrecergacriceaca **IGGTCGACGTGGACCGAGTGGTCCG** CGCACCCGGACCTGCACCAACCCCG AATGTCCATGACCGCACCGTCTCCT saggirciccideagigeedeedee CGGAACGAGGACCTGGTGGACCCGT AGAATGAGGATGTCATCGACCCCA AGCCTGGTGGTGCGACAGGCCCGCC Accicarcarcéecaseces AACATCGTGGCACGTCGCCGCAGCG recreacrescasadresicae CGGAGCCGGAGCTGCACCAACCCGG SCATTCCAGAA---GACCGCCTGCA

7;

102;

0; Mismatches 961; Score 887.4; DB 6; Pred. No. 3.8e-154;

Length Indels

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30.8%;

Best Local Similarity 60.6 Matches 1636; Conservative

Query Match

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TCTCTATGGACCGGTACCTGAATTACTTTGCCACCAAAGCGAGGCCCCACGGGTGTGATCC 2741
                                                               2786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     storage disorder; muscle disorder; neurodegenerative disorder; nootropic; developmental defect; neuroprotective; antiparkinsonian; hypotensive; hypotensive; haemostatic; cardiant; antianginal; dermatological; immunosuppressive; antianflammatory; virucide; antibacterial; anti-HIV; antiparastic; antiallergic; antidiabetic; immunomodulator; antipsoriatic; vulnerary; anorectic; antidiabetic; immunomodulator; antipsoriatic; antiphrotropic; kerolytic; antiulcer; cerebroprotective; anticonvulsant; antiinferiulity; antimanic; antidepressant; metabolic; cytostatic;
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                                                                                                                     2742 Tegaccircressaadcrerecadeacadaresearcereareaceresearecer
                                                                                                                                                                                 TGGCTGGACTGGGCCAGCCAGCCAGCTGTCACAGTGTCGGAGGCTGAGTGCTGA
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The present invention provides the protein and coding sequences of several novel human proteins, designated NOVX. These can be used in the treatment of, amongst others, cancers, autoimmune diseases, infections, inflammatory diseases, storage disorders, muscle disorders, neurodegenerative diseases and developmental defects. The present

Sequence 2860 BP; 557 A; 950 C; 858 G; 495 T; 0 U; 0 Other; is a coding sequence of the invention

sednence

or

Novel isolated polypeptide, designated NOVX, useful for treating preventing in NOVX-associated disorders e.g. cardiomyopathy, atherosclerosis, diabetes, cancer, allergy, asthma, Crohn's disea

2002-590741/63.

P-PSDB; AA018735

Claim 9; Page 14; 353pp; English.

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skin disorder; infectious disease; anorexia; behavioral disorder; valve disease, endocrine disorder; heart disorder; blood disorder; anxiety disorder; brain disorder; inflammatory disorder; neurodegenerative disorder; Alzhaimer's disease; parkinson's disease; immune disorder; haematopoietic disorder; dyelipidaemia; metabolic disturbance; obesity; metabolic syndrome X; wasting disorder; gene therapy; transgenic animal; human; gene; ds.

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2000US-0238397P

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Zerhusen BD, Mezes PS; Alsobrook JP, Lepley DM; V, Ellerman K, Macdougall on G, Szekeres ES;

Gerlach V, El

Burgess CE, Grosse WM,

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Li L, Edinger S, Ge
Millet I, Stone D,
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P-PSDB; ABG61795.
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                                             Shimkets RA,
Rastelli L, P
Spytek KA, L:
Gunther E, M:
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The invention describes an isolated polypeptide (I), useful in the manufacture of a medicament for treating a syndrome associated with a human disease. (I), the polymucleotide encoding it (II) and an antibody (III) to (I) are useful for treating or preventing cancer, metabolic disorders, skin disorders, infectious disease, anorexia, behavioral disorders, anxiety disorders, brain disorders, heart and blood neurodegenerative disorder, Alzhaimer's disease, Parkinson's disorder, immune disorders, anxiety disorder, Alzhaimer's disease, Parkinson's disorder, immune disorders, hematopoietic disorders, and the various dyslipidaemias, metabolic disturbances associated with obtaining disorders, immune disorder, and the metabolic syndrome X and wasting disorders associated with chronic diseases. (I), (II) or (III) are useful in screening assays, decetion predictive medicine (e.g., therapeutic assays), and in methods of treatment (e.g., therapeutic assays), in methods of treatment (e.g., therapeutic assays), and useful as immunogen to produce antibodies immunospecific for (I) to screen for potential agonist and antagonist compounds, and as bait protein in a two-hybrid or three-hybrid assay. (II) is useful in gene therapy, to express (I), to detect (I) mana quentic lesion in a (I) therapy, to express (I), to detect (I) mRNA or a genetic lesion in a (I) gene, and to modulate activity of (I). A cell containing a vector exressing (I) is useful for producing non-human transgenic animals. This encodes a novel human polypeptide described in the invention or Novel isolated polypeptide, designated NOVX, useful for treating of preventing cancer, diabetes, obesity, dyslipidemia, anorexia, and metabolic, neurodegenerative, immune and hematopoietic disorders. Claim 9; Page 93; 316pp; English.

Sequence 2995 BP; 571 A; 984 C; 925 G; 515 T; 0 U; 0 Other;

143 214 157 203 274 263 334 CCGCTGCCGCGCCTTCCCCGCCACATCTTCAAGTGCAACGGCGAGTGGGTCAG 323 ----TGATCGAGCGCAGCACAGACGGGAGCAGTGG 379 97 83 CCGCCCGCGGGGCCCCGCCGGCCCGCCTGCCCGCCGCGCGCCATGGCCGTCCG cadocorredededasasececeses con consequences de GCCCTACTTCCTGCAGGGCCACAGGACGCCTACATTGTGAAGAACAAGCCTGTGGAAGCT GCCCGGCCTGTGGCCTCCTGGCCATAGTCCTCGCCGCTTGGCTCCGCGGCTCGGG TCGGGCGCGCTGCTGCTGCTGCTGCTCTGCTGGGACCCGAGGCTGAGCCAAGCAGG 275 TGTGTGCAAGGCCGTGCCCGCCACGCAGATCTTCTTCAAGTGCAACGGGGAGTGGGTGCG TGCCCAGC---AGAGTGCCACCGTGGCCAACCCAGTGCCTGGTGCCAACCCGGACCTGCT raggandecancedericaegracioneceralecentecentes de la secondecente desente de la secondecente de la secondecente de la secondecent TCCCCACTTCCTGGTGGAGCCCGAGGATGTGTACATCGTCAAGAACAAGCCAGTGCTGCT Gaps Indels 138; Length 2995; Score 875.8; DB 6; Pred. No. 5.3e-152; 0; Mismatches 1022; ; 0 CCAGGTGGACCACG-----Query Match
Best Local Similarity 59.8%;
Matches 1727; Conservative 215 38 98 158 144 204 335 Query Match

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1039 1040 1099 1160 439 443 499 559 619 1100 CACCACCACCTACCAGGGCAGTCTCTGTCCCGGCAGGATGGGCCCAGCCCCAAGTT 1429 503 563 623 619 683 739 743 799 803 859 863 919 923 979 GCTGGAGGAATACTGGTGCCAGTGCGTGGAGCTCCTCGGGCACCACCAAGAGTCA 380 TGAGCCGACCATGGAGGTCCGCATTAATGTCTCAAGGCAGCAGGTCGAGAAGGTGTTCGG CCTGCGGGTGCGCGAGGTCGAGGTCGAGGTCGCGCAGCAGGAGGAGGAGCTCTTTGG 500 GAAGGCCTACATCCGCATAGCCAGATTGCGCAAGAACTTCGAGCAGGAGCCGCTGGCCAA 504 ccgadccracgrccccrarcrcccracagaacrrcgarcagagaccrcraggaga GGAGGTGTCCCTGGAGGAGCATCGTGCTGCCCTGCCGTCCACCGGAGGGCATCCCTCC ATACATCACGCGGGAGCACAGCCTGGTGGGGCGACAGGCCCGCCTTGCTGACACGGCCAA CTACACCTGCGTGGCCAAGAACATCGTGGCACGTCGCCGCAGCGCCTCCGCTGTCAT AGCCGAGGTGGAGTGGCTCCGGAACGAGGACCTGGTGGACCCGTGGACCCCAATGT craracciecaredecaredarcaredecaaaceceaacecaccaccaccerear CGTCTACGTGAACGGTGGTCGACGTGGACCGAGTGGTCCGTCTGCAGCGCCCAGCTG cercracerearrecercerecreecedeacacacerecerecerecerecere TGGGCGCGCGCCAGAAACGGAGCCGGAGCTGCACCAACCCGGCGCCTCTCAACGGGG TGGCCGAGGCTGGCAGGCGCACCCGGACCTGCACCCCGCTCCACCTCAACGGAGG GGACGGCAGCTGGAGCCCGTGGAGCAAGTGGTCGGCCTGTGGGGCTGGACTGCACTG GCGGAGCCGTGAGTGCTCTGACCCCAGCAACGGAGGGGAGGAGTGCCAGGGCAC 1041 GCGTAGCCGCGAGTGCATGCCCCCCCACCCCAGAACGGAGGCCGTGACTGCAGCCGGAC GCTGCTCGÁCTCTAAGAÁCTGCACAGATGGGCTGTGCATGCAAAGTGAGCCTGTCCCGC TAAGACGGCAAGGCCCAGTAACCCGCAGCTCCTACACCCCTCTGTGCCTCTGACCTGAC CGCTTTCTGTGAGGGCAGAATGTCCATGACCGCACCGTCTCCTCTCTGTTGTCTCTGT 924 Géccrircrigadadegecadecarricadaa---Gaccecerecaccarcreceaer 1100 TGACCTGGACACCCGCAACTGTACCAGTGACCTCTGTGTACACAGTGCTTCTGGCC----CTGAGGACGTGGCCCTCTATGTGGCCCTC---ATCGCCGTGGCCGT GGTCGTGGCAATCCTCATGGCGGTGGGTGGTGTGTACCGCCGCAACTGCCGTGACTT --CTCACCTCAGGCTTCCAGCCCGTCAGCAT CGACACAGACATCACTGATCTGCTGCTGACTGGTTTTCCACCCCGTCAACTT CAAGCCCAGCAAAGCAGACAACCCCCATCTGCT-----CACCATCCAGCCGGACCTCAG 1161 AGTGCTGGAGGCCTCAGGGGATGCGGCGCTGTATGCGGGGCTCGTGGTGGCCATCTTCGT CIGCCIGGICCIGCIGCTGCTTGTCCTCATCCTCGTTTATTGCCGGAAGAAGAAGAAGACGCT GGACTCAGATGTGGCTGACTCGTCCATT-324 440 620 260 684 744 800 920 980 740 804 860 1040 1101 1156 1199 1221 1259 1281 1316 1370 d ò à q à a à d à g à 셤 ö g à qq ⋧ g ά ద g à à 셤 qq ò à d ò g à 임 ð Ωp ò

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Human; NOVX; neurological disorder; Alzheimer's disease;

KW Huttington's disease; Parkinson's disease; pain; behavioural disorder;

KW Huttington's disease; Parkinson's disease; pain; behavioural disorder;

KW addiction; tuberous scalerosis; cancer; immune disorder; allergy;

KW thyroiditis; cardiovascular disease; hypertension; reproductive disorder;

KW thyroiditis; cirrhosis; glomerular endotheliosis; bacterial infection;

KW polycystic kidney disease; endocrine disorder; obesity; cardiomyopathy;

KW atherosclerosis; cell signal processing-related disorder;

M metabolic pathway regulation disorder; cytostatic; neuroprotective;

KW dermatological; antibacterial; antiarthrito; hepatotropic; neuroprotective;

KW defiferentiation; proliferation; motility; haematopoiesis; wound healing;

KW adjogenesis; forensic biology; transgenic animal; drug screening;

KW gene therapy; NOV11; transmembrane receptor UNCSH2-like; chromosome 10;
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                        CTTCAACATCACCAAGGACA---CAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGC
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05-JAN-2001; 2001US-0260018P.

08-JAN-2001; 2001US-0250360P.

28-FEB-2001; 2001US-0272411P.

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                                                                           Gorman
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(CURA-) CURAGEN CORP.

P, Tchernev VT, Liu X, Spytek KA;

MM, Lepley DM, Burgess CE, Vernet CAM, Li L;
Sciore P, Ellerman K, Malyankar U;
Sciolog F, Guo X, Shenoy S, Anderson D;
J, Miller CE, Eisen A; Kekuda R, Alsobrook JP, Patturajan M, Grosse WM, Gorman L, Edinger S, Sc. Rothenberg M, Stone D, Padigaru M, Taupier RJ,

WPI; 2002-583619/62 P-PSDB; ABB09520. Novel polypeptides and nucleic acids homologous to transmembrane receptor, thymosin, neuromodulin-like family of proteins for diagnosing, treating cancer, atherosclerosis, neurological, skin and autoimmune disorders.

Claim 9a; Page 121; 323pp; English

The invention relates to 24 novel human proteins designated NOV1-NOV14

(ABB09501-ABB09524), collectively referred to as NOVX proteins, and
nucleic acides encoding them (AB03897-AB03902). NOVX proteins and
nucleic acides encoding them (AB03897-AB03902). NOVX proteins and
nucleic acides encoding them (AB03897-AB03902). NOVX proteins are
nucleic acides encoding them (AB03897-AB03902). NOVX proteins are
succiated disorders or in the manufacture of a medicament for treating
such disorders with specific applications described for each of the 24
NOVX proteins, based on their homology to known proteins. Various
CC disorders are associated with NOVX proteins including neurological
disorders and autoimmune diseases), mysathenia gravis, asther
cc disorders and autoimmune diseases, physathenia gravis, asther
cc e.g., hypertension), reproductive disorders, endometriosis,
various forms of arthritis, diabetes, thyroiditis, cardiovascular disease
(e.g., hypertension), reproductive disorders, endometriosis,
incontinence, psoriasis, scleroderma, alopecia, ulcers, pancreatitis,
incontinence, psoriasis, scleroderma, alopecia, ulcers, pancreatitis,
disorders, obseiry, bacterial infections and particularly ardiomyopathy
atherosclerosis, cell signal processing-related disorders and disorders
cof metabolic pathway regulation. NoVX nucleic acids and polypeptides may
albends to a NOVX protein, and are also useful as targets for the
as neurogenesis, cell differentiation, cell motility a cell or tissue type and
are useful as a source of primers or probes for forensic biology and for
identifying and cloning NOVX homologues in other cell types. Cell
comprising NOVX nucleic acids are useful for producing non-human
transgenic animals which are useful for producing cell type acining NOVX proteins and for identifying and evaluating models acutive The gene encoding NOV11 transmembrane receptor UNC5H2-like protein NOV11.

Sequence 2895 BP; 557 A; 960 C; 854 G; 524 T; 0 U; 0 Other;

Indels 138; Gaps Score 866.4; DB 6; Length 2895; Pred. No. 2.8e-150; 0; Mismatches 941; Indels 138; 30.1**%**; 60.6**%**; Best Local Similarity 60.6 Matches 1659; Conservative Query Match

ολ	- G	CAGTGCCTGGTGCCAACCCGGACCTGCTTCCCTGGTGGAGCCCGAGGATG 243
qa	40 ACT	
Qy	244 TGTA(	CATCGTCAAGAACAAGCCAGGCTGCTTGTGTGCAAGGCGGTGCCGGCACGCAGGA 303
Dp	200 CCIA	ATTGTGAAGAACAAGCTGTGGAGCTCCGCTGCCGCGCCTTCCCCGCCACACAGA 25
ò	1 40 T	CTICITCAAGIGCAAAGGGGAGIGGGGCGGGGGGGGGGGG
QQ	260 rcrA	31
ð,	364 CAGA	42
qu	320 TGGA	TGGATGAGGCCACCGGTCTGCGGGTGCGAGGTCGAGGTCGAGGTCGCGGGAGCAGCAGG
δy	424 TCGA	48
DP	380 TGGA	43
ò	484 GCAC	GCACCACCAAGAGTCAGAAGGCCTACACTCCGCATAGCCAGATTGCGCAAGAACTTCGAGC 543
СР	440 GCAC	ر 1 49
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Qy	604 CGGA	GGGCATCCCTCCAGCCGAGGTGGAGTGGCTCCGGAACGAGGACCTGGTGGACCGT 663
qq	1111 560 CGGA	CGGAGGGGGGCCTGGCCCGAGGTGGAATGGCTCAAGAATGAGGATGTCATCGACCCCA 619
δy	664 CCCT	3GACCCCAATGTATACATCACGCGGAGACACCTGGTGGTGCGACAGGCCCGC
Db	_ပ	33ACACCAACTICCIGCTCACCAICGACCACAACCICAICAICTCGCCAGGCCCGCC 6
٥٧	724 TTGC	TGACACGGCCAACTACACCTGCCTGGCCAAGAACATCGTGGCACGTCGCCGCGCGGGG 783
Db	680 TGTC	TGTCGGACACTGCCAACTATACCTGCGTGGCCAAGAACATCGTGGCCAAACGCCGGAGCA 739
Qy	784 CCTC	GGTGCTGTCATCGTCTACGTGAACGGTGGTCGACGTGGACGAGTGGTCCG 843
qq	740 CCAC	CTGCCACCGTCATCGTCTACGTGAATGGCGGCTGGTCCAGCTGGGCAGAGTGGTCAC 799
δý	844 TCTG	CAGCGCCAGCTGTGGGCGGCTGGCAGAACGGAGCCGGAGCTGCACCGGG 903
Dp	800 CCTG	CTGCTCCAACCGCTGTGTGTGTGTGTGTGTGTGTGTGTGT
ò	904 CGCC	ICTCAACGGGGGCTTTCTGTGAGGGCAGAATGTCCATGACCGCACCGTCTCCT 963
Db	860 CTCC	CICCACTCAACGGAGGGCCTTCTGCGAGGCCAGGCATTCCAGAAGACCGCCTGCA 916
Οy	964 CTCT	CTGCTTGTCTCTGTGGACGGCAGCTGGAGCCGTGGAGCAAGTGGTCGGCCTGTGGGC 1023
Db	917 CCAC	CCATCTGCCCAGTGGAGGGGGGGAGGGAGGGGAAGTGGTCAGCCAGC
δλ	1024 TGGA(	TIGCACCCACTIGGGGGGGGGCGTGGGTCTGACCCAGCGCCCCAACGGAGGGG 1083
QQ	977 CTGAC	CTGAGTGTGCCCACTGGCGTAGCCGCGAGTGCATGGCGCCCCCACCCCAGAAGGGCC 1036
Ολ	1084 AGGAC	STGCCAGGGCACTGACCTGGCACCGCAACTGTACCAGTGACCTCTGTGTACACA 1143
Db	1037 GTGAC	GTGACTGCAGCGGGACGCTGCTCGACTCTAAGAACTGCACAGATGGGCTGTGCATGCA
ζŏ	1144 GTGC7	TTCTjdgcccrqagqacgrggccc 1170
qq	1097 GTGAC	
οχ	1171 TCTAT	TCTAIGIGGCCTCAICGCCGIGGCCGICTGCTGGTCCTGCTGCTGCTGCTTGTCCTCA 1227
QQ	1157 TGTAT	GCGGGCTCGTGGTGCTTCGTGGTGGTATCCTCATGGCGTGGGGG 1216

		2155 GCGGATACTTGGTGGGAGGCCGAAACGCTTCTGAACTTACACAACCTGC 2237 2234 GCGGATACTTGGTGGAGGAGGCCGAAACGCTTATTCAAGGACAACCTGC 2293 2215 GCCTATCCATCACGATGTGCCCAGCTCCTGTGGAAGGTAAGCTCCTTGTCAGCTACC 2274
Text		
1286  1276  0y		
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1286 Db 2294 1276 Oy 2275	2354	133
1286 Db 2294	. 2275	TGGTGGTGTACCGCCGCAACTGCCGTGACTTCGACAACAGCATCACTGACTG
	2294	TCCTCGTTTATTGCCGGAAGGAGGGCTGGACTCAGATGTGCTGACTCGTCCATT-

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2473 2533 2511 2593 2631 2334 2413 CTTCAAGATCCCCTTCCTCATTCGGCAGAAGATAATTTCCAGCCTGGACCCACCTGTA 2571 Caccididection de la comparta de la nerringeerechadecechaecechentearecrenhaecergegaggegegegen 2691 ccracagecarercagececasecaragasecracecagecarecagecagecages 2451 TTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGTCCCAGCCCTGGTGGGCCCCCAGTG ccresadadecadascresecresadascresadascresadascresadadas ogcogogracocacinos con contra AGGAGATCCCCTTTTATCACATCTGGAATGGCACGCAGCGGTACTTGCACTGCACCTTCA TGGAGGGCGACAGAGCTTCAGCATCAACTTCAACATCACCAAG----GACACAAGGT CTGGCCTCTTCACAGTGTCGGAGGCTGAGGC 2789 rgcrggrgcrgrggccaccgacgggacrgcrgagcc 2871

Search completed: October 5, 2004, 15:38:48 Job time : 1125 secs us-09-970-944-1.rni

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LENGTH: 3014 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
8312
1288
2211
22211
2289
1627
7218
1951
1951
453
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Best Local Similarity 88.5
Matches 2474; Conservative
                                                                                                           11220
36778
38506
38506
38506
1065
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USA
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STATE: CA
COUNTRY:
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Sequence 1, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 1806, Ap
Sequence 3, Appli
Sequence 1807, Ap
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Sequence 38, Appli
Sequence 38, Appl
Sequence 7947, Ap
Sequence 7533, Ap
Sequence 7533, Ap
                                                                   October 5, 2004, 15:11:27 ; Search time 199 Seconds (without alignments) 8034.239 Million cell updates/sec
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Sequence 12126, A
Sequence 12292, A
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Sequence 39, Appl
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/cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/pcTUS_COMB.seq:*
     GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-09-306-902A-1
US-09-306-902A-2
US-09-333-381-1806
US-09-333-381-1806
US-09-306-902A-3
US-09-306-902A-3
US-09-833-381-1807
US-09-833-381-1807
US-09-803-38-1
US-09-253-991A-7947
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US-09-252-991A-72265
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US-09-252-991A-9933
US-09-252-991A-10142
US-08-690-473-1
US-09-259-821A-1
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                                                                                                                                                                                            682709 segs, 277475446 residues
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Listing first 45 summaries
                                                 - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Sequence 11256, A Sequence 11095, A Sequence 11, Appl Sequence 14, Appl Sequence 1, Appli Sequence 1, Appli Sequence 3771, Appli Sequence 1, Appli Sequence 1, Appli Sequence 3971, Ap Sequence 4004, Appl Sequence 32, Appli Sequence 19, Appli 4 87 ATGGCCGTCCGGCCCGGCCTGTGGCCAGCGCTCCTGGCCATAGTCCTCGCCGCTTGGCTC 146 Gaps Sequence Sequence 11; 0; Mismatches 312; Indels SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/808,982 DB 2; US-09-252-991A-11256 US-09-252-991A-10995 US-09-675-018B-11 US-08-222-463-14 US-08-922-865-11 US-09-510-949-1 US-09-252-991A-3971 US-09-252-991A-3971 US-09-252-991A-3074 Sequence 1, Application US/08808982
Fatent No. 5939271
Fatent No. 5939271
Fatent No. 5939271
FAPLICANT: Tessier-Lavigne, Marc
APPLICANT: Hink, Lindsay
APPLICANT: Hink, Lindsay
APPLICANT: Kazuko, Keino-Masu
TITLE OF INVENTION: Netrin Receptors
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAM GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITTY: SAN FRANCISCO
STATE: CALIFORNIA US-09-657-440-19 US-09-340-798A-31 US-09-105-537-5 US-09-320-878-19 US-09-141-908-1 US-07-951-715A-6 US-08-459-448A-6 77.6%; Score 2235.8; 88.5%; Pred. No. 0; ALIGNMENTS UC96-217 ZIP: 94104 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS\_DOS FILLING DATE:
CLASSIFICATION: 530
ATTORNEY AGENT THYORMATION:
NAME: OSMAN, RICHARD A,
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: UC96.
TELEFONMUNICATION INFORMATION:
TELEFANS (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:

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9 <u>2</u> 5	5 8 5 8	CTC 16
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                                                                                                                                                                                                                        Length 3014;
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                                                                                                                                                                                                                   Score 2235.8;
Pred. No. 0;
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                    TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3014 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
                                                                                                                                                                  ; SEQUENCE DESCRIPTION: SEQ ID NO: US-09-306-902A-1
        TELECOMMUNICATION INFORMATION:
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Best Local Similarity 88.5%;
Matches 2474; Conservative
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GGCACGCAGCGGTACTTGCACTGCACCTTCACCTGGAGCGTGTCAGCCCCCAGCACTAGT 2363
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                    2395 GGGGTCCCACCCGCTGGTGGCCCCCAGTGCCTTCAAGATCCCCTTCCTCATTCGCCAAAAG
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/306,902A
FILING DATE: 07-May-1999
CLASSIFICATION: <UNknown>
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TITLE OF INVENTION: Netrin Receptors
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSE: SCIENCE & TECHNOLOGY LAW GR.
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: UC96-217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Tessier-Lavigne, Marc
Leonardo, E. David
Hink, Lindsay
Masu, Masayuki
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Patent No. 6277585
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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                                                                                                                                           SOFTWARE: STATEMENT FOLOSOFIA: SOFTWARE: CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/808,982
FILING DATE: CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION: NAME: OSMAN, RICHARD A REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: UC96-217
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T: 268 BUSH STREET, SUITE 3200
SAN FRANCISCO
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Pred. No. 0;
0; Mismatches
              ADDRESSEE: SCIENCE & TECHNOLOGY LAISTEET: 268 BUSH STREET, SUITE 320 CITY: SAN FRANCISCO STATE: CALIFORNIA COUNTRY: USA ZIP: 94104 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE OF SYSTEM: PC-DOS/MS-DOS COMPUTER: SYSTEM: PC-DOS/MS-DOS COMPATING SYSTEM: PC-DOS/MS-DOS COMPATING SYSTEM: PC-DOS/MS-DOS COMPATING SYSTEM:
                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1787 base pairs
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Matches 1721; Conservative
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STRANDEDNESS: double
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MOLECULE TYPE: CDNA
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US-08-808-982-2
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ADDRESSE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
STREET: CALIFORNIA
COUNTRY: USA
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                                                                                                                                          GAAGCCGGACAGGGCCCTTCCCCCACACGGGGAGA
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTHARE: Patentin Release #1.0, V6
SURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/306,902A
FILLING DATE: 07-May-1999
CLASSIFICATION: <a href="https://documents.com/">UNKDOWN></a>
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96.9%; Pred. No. 0;
iive 0; Mismatches
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TITLE OF INVENTION: Netrin Receptors
NUMBER OF SEQUENCES: 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (415) 343-4341
TELEPAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/09306902A
Patent No. 6277588
GENERAL INFORMATION:
APPLICANT: Tessier-Lavigne, Marc
Leonardo, E. David
Hink, Lindsay
Masu, Massy, Massu,
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REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: UC
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy disk
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Best Local Similarity 96.9
Matches 1721; Conservative
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US-09-306-902A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    483
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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Pred. No. 5.7e-161;
0; Mismatches 971;
                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Tessier-Lavigne, Marc
APPLICANT: Leonardo, E. David
APPLICANT: Hink, Lindsay
APPLICANT: Hank, Lindsay
APPLICANT: Kazuko, Keino-Masu
TITLE OF INVENTION: Netrin Receptors
INWHERE OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GR
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
                                                                AGTGTCGGAGGCTGAGTGCTGAGGCCGG
                        AGTGTCGGAGGCTGAGTGCTGAGGCCGG
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: CORMAN, RICHARD.
REGISTRATION NUMBER: 36,627
REPRECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION NFOREMATION:
TELEFAX: (415) 343-4341
TELEFAX: (415) 343-4341
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERIFICS:
LENGTH: 2831 base pairs
                                                                                                                                                                                                                                                                                         Sequence 3, Application US/08808982
Patent No. 5939271
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27.2%;
Best Local Similarity 59.4%;
Matches 1625; Conservative
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STRANDEDNESS: double
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                                                                      GGGGGGGTGCCGACTCTGGCCCAGAAACTCCACCTGGACAGCCATCTCAGCT
                                                                                                                                                        2617 CACGGGGCAATGACTGGCGGCTGTTGGCACAGAAGCTCTCCATGGACCGGTACCTGAACT
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/306,902A
FILING DATE: 07-M9-1999
CLASSIFICATION: CURROWN>
ATTORNEY/AGENT INFORMATION:
NAMME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: UC96-217
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP STREET: 268 BUSH STREET, SUITE 3200 CITY: SAN FRANCISCO
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59.4%; Pred. No. 5.7e-161;
ilve 0; Mismatches 971;
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OF INVENTION: Netrin Receptors
R OF SEQUENCES: 9
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US-09-306-902A-3
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Hink, Lindsay
Masu, Masayuki
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
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STRANDEDNESS: double
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US-09-306-902A-3
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2017
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1966 TCTTCACCGAGCAGCTGGGCCGCTTTGCCCTGGTGGGAGGGCCCTCAGCGTGGCTGCCG 2025
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     221 CCATCCACGATGTGCCCAGCTCCCTGTGGAAGAGTAAGCTCCTTGTCAGCTACCAGGAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 regardadedeccreaacacacccrecracre-caccrecaedeccre-raca
                                                   262 recrecchigacerececengecentigaagaagaagengeregeeaannacaagaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4.1%; Score 119; DB 2; Length 305; 58.1%; Pred. No. 5.6e-17; Ive 0; Mismatches 95; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/808,982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SSEE: SCIENCE & TECHNOLOGY LAW GROUP
F: 268 BUSH STREET, SUITE 3200
SAN FRANCISCO
                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/08808982;
Patent No. 5939271
GENERAL INFORMATION:
APPLICANT: Teesier-Lavigne, Marc
APPLICANT: Hennardo, E. David
APPLICANT: Hink, Lindsay
APPLICANT: Masu, Masayuki
APPLICANT: Kazuko, Keino-Masu
TILLBOF INVENTION: Netrin Receptors
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: UC94
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36,627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ilarity 68.1%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            305 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleic acid
EDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CALIFORNIA
USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 209; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                 2341 AGCG 2344
                                                                                                                                                                                                                                                                     144 AGAG 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
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                                                                                                             2281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    618 AGACCCAGGCCCACCAGGGCCACTGGG---AGGAGGTGGTGACCCTGGATGAGGAGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1921 CCTCCCACCTCTACTACTGCCAGCTGGAGGCCAGTGCCTGCTACGTCTTCACCGAGCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         561 reaacacacccrecracracraccaecreeaecccaeeeccrercacarccrecreeredaccaec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2041 IGCTTCTGTTTGCGCCGGTGGCCTGCACCTCCCTCGAGTACAACATCCGGGGTCTACTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      441 TGGCCGTCTTCGCCCCCCCCTCTGCACCTCCCTGGAGTACAGACTCCGGGTCTACTGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             738 AGACAGIATTGAGCCCCTCGGTGACCTGTGGACCCACAGGCCTCCTGCTGTGCCGCCCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1801 TCATCCTGGCTATGGACCACTGTGGGGGGCCCAGCCCTGACAGCTGGAGCCTGCGCCTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               678 TCATCCTCACCATGCCCCACTGTGCCGAAGTCAGTGCCCGTGACTGGATCTTTCAGCTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1861 AAAAGCAGTGGGGAGGGCAGCTGGGAGCAGGATGTGCTGCACCTGGGCGAGGAGGCGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 8.9%; Score 256; DB 1; Length 77 Best Local Similarity 67.2%; Pred. No. 1.3e-46; Matches 406; Conservative 1; Mismatches 191; Indels
APPLICANT: Gyuris, Jeno
APPLICANT: Gyuris, Jeno
APPLICANT: Draetta, Giulio
TITLE OF INVENTION: CDK4 Binding Proteins
NUMBER OF SEQUENCES: 95
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/253,155A
FILING DATE: 02-UUN-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Vincent, Matthew P.
REGISTATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MII-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEPAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 771 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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US-08-253-155A-17
                                                                                                                                                                                         STREET: 60 St.
CITY: Boston
STATE: MA
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2146 AGCAGCTGGGGGACAGCTGATCCAGGAGCCACGGGTCCTGCACTTCAAGGACAGTTACC 2205
119 TCAAGCGGCTCCAGCTGGCCGT-TTCGCCCCCCCCTCTGCACCTCCCTGGAGTACAGCC 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66 CCCGCCIGCCCGCCGCCGCCAIGGCCGTCCGGCCCGGCCTGIGGCCAGCGCTCCTGGGC 125
                                              2086 ICCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAGGTGGTGCAGCTGGAGA
                                                                                                                                                                                  238 GGACTCTGGGCGGATACTTGGTGGAGGAGCCGAAACCGCTAATGTTCAAGGACAGTTACC
                                                                                          6 GGGCTCCGGGCTGAGGCGCTTAAAGCCGCCTCCCGCGGGGGCCCCGGGGGCCCCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ch 1.8%; Score 51.8; DB 3; Length 1280; 18 Similarity 51.0%; Pred. No. 0.034; 122; Conservative 0; Mismatches 117; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Murray & Borun
                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Roizman, Bernard
APPLICANT: Roizman, Bernard
APPLICANT: Chou, Joany
TITLE OF INVENTION: Method for Treating Tumorigenic
TITLE OF INVENTION: Diseases
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: Marshall, O'Toole, Gerstein, Murray & 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28097/32742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/483,533
FILING DATE: 07-MAR-95
FILING STETCATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/419,853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                Sequence 38, Application US/08483533 Patent No. 6172047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 11-APR-95
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/861,233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 28,491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 2
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: DNA (genomic) US-08-483-533-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 31-MAR-92
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : 312/474-6300
312/474-0448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 25-3856
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zeller, James P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       single
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                                                                                                                                                                                                                                                                                                                                                    RESULT 12
US-08-483-533-38
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Best Local 8
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                                                     178 rccedercracrecresagacacecrerarecacherasagacecresage 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1966 ICTICACCGAGCAGCTGGGCCGCTTTGCCCTGGTGGGAGAGGCCCTCAGCGTGGCTGCCG 2025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2026 CCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGCCTGCACCTCCTCGAGTACAACA 2085
                                                                                                                                                238 GARCTCTGGGCGGATACTTGGTGGAGGAGCCGAAACCGCTAATGTTCAAGGACAGTTACC 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59 TCCTGCTGGACCAGCTGGGCACCTATCATTCACGGGCGAGTCCTATTCCCGCTCAGCAG 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rádardaddadcecreaacacacecreciacia-caderiddadececadddecerd-raea sa
         2086 ICCGGGTCTACTGCCTGCATGACACCCCACGATGCACTCAAGGAGGTGGTGCAGCTGGAGA
                                                                                                    2146 AGCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCCTGCACTTCAAGGACAGTTACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 305;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95; Indels
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MEDIUT ATDABLE FORM:
MEDIUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP STREET: 268 BUSH STREET, SUITE 3200 CITY: SAN FRANCISCO STATE: CALIFORNIA COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 119; DB 3;
Pred. No. 5.6e-17;
0; Mismatches 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/09/306,902A FILING DATE: 07-May-1999 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Tessier-Lavigne, Marc
Leonardo, E. David
Hink, Lindsay
Masu, Masayuki
Kazuko, Keino-Masu
TITLE OF INVENTION: Netrin Receptors
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-306-902A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: UC
TELECOMMUNICATION INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (415) 343-4341
                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/09306902A
Patent No. 6277585
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 305 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 4.1%;
Best Local Similarity 68.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 209; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (415)
                                                                                                                                                                                                 2206 ACAACCT 2212
                                                                                                                                                                                                                                             298 ACAACCT 304
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Sequence 7809, Application US/09252991A

Patent No. 6551795
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rubenfield et al.
NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2116 ATGCACTCAAGGAGGTGGTGCAGCTGGAGAAGCAGCTGGGGGGAACAGCTGATCCAGGAGC 2175
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615 ACCCCCGCGACCCCCCGCGACCCCCCGCGCGGGTGCGCTTCTCGCCCCACGTC 674
                                                                           126 ATAGICCICGCCGCTIGGCTCCGCGGCTCGGGTGCCCAGCAGAGTGCCACCGTGGCCAAC 185
                                                                                                                                  cassinacaccaccidaragaccircaaccaccicaccidacacacacacacacacacacacara 734
                                                                                                                                                                                                                                                             168 accacerciaccacaaccaaccacercicaccaaccaacciacciarcciaccacariccec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT APPLICATION NUMBER: US/09/252,991A PRIOR PILING DATE: 1999-02-18 PRIOR FILING DATE: 1998-02-18 PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR APPLICATION UNDER: US 60/094,190 NUMBER: US 60/094,190 NUMBER OF SEQ ID NOS: 33142
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Best Local Similarity 47.5%;
Matches 152; Conservative
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APPLICANT: Marc J.
TITLE OF INVENTION:
TITLE OF INVENTION:
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US-09-252-991A-7947
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                 ATAGTCCTCGCCGCTTGGCTCCGCGGCTCGGGTGCCCAGCAGAGTGCCACCGTGGCCAAC 185
                                                                                                                                                                                     675 ceacinececenterregrenterrecenterios contra cont
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Pred. No. 0.034;
0; Mismatches 117; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Treating Tumorigenic Diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: Marshall, O'Toole, Gerstein, Murray & Borun 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Comparible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CAPENT APPLICATION DATA:
APPLICATION NUMBER: US/09/283,471A
FILING DATE: 04-APR-1999
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Y: United States of America
60606-6402
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CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/861,233
FILING DATE: 31-MRR-1992
PRIOR APPLICATION DATA:
FILING DATE: 11-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/419,853
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 13
US-09-283-471A-38
; Sequence 38, Application US/09283471A
; Patent No. 6340673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Rolzman, Bernard
APPLICANT: Chou, Joany
TITLE OF INVENTION: Method For V
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Zeller, James P. REGISTRATION NUMBER: 28,491
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TELEPHONE: 312/474-6300
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Best Local Similarity 51.0%;
Matches 122; Conservative
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INFORMATION FOR SEQ ID NO:
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MEDIUM TYPE: Floppy
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STREET: 62...
-w. Chicago
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STATE: 11
COUNTRY:
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1876 AGGGCAGCTGGGAGCAGGATGTGCTGCACCTGGGGGAGGGGGCGCCTCCCACCTCTACT 1935
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                                                                                                                                                                                                                                                                                                      428 AcGACCTGGTGGTGCCCAGCGACAGCTTCCTGCCCAACTACCTGAAGGCCGAGGTGTTCC 487
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                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                      Query Match
1.8%; Score 51.2; DB 4; Length 1302;
Best Local Similarity 47.5%; Pred. No. 0.046;
Matches 152; Conservative 0; Mismatches 168; Indels 0.
PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR FILING DATE: 1998-02-18 PRIOR PRING APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27 NUMBER OF SEQ ID NOS: 33142 SEQ ID NO 7809 LENGTH: 1302
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                                                                                                                            TYPE: DNA
CRGANISM: Pseudomonas aeruginosa
US-09-252-991A-7809
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Search completed: October 5, 2004, 20:46:56 Job time: 210 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model	: October 5, 2004, 15:20:19 ; Search time 1321 Seconds (without alignments) 11056.338 Million cell updates/sec	US-09-970-944-1 t score: 2881 ce: l agctgggggtcggggctgagccttccccacaccggggaga 2881	<pre>g table: IDENTITY NUC</pre>
OM nucleic - 1	Run on:	Title: Perfect score: Sequence:	Scoring table:

3340653 seqs, 2534783454 residues Searched:

6681306 Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries seq length: 0 seq length: 2000000000 Minimum DB Maximum DB

Applications NA:\* Published Database

'(cgn2\_6/ptodata/2/pubpna/US07\_puBCOMB seq:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Sequence 1, Appli Sequence 1, Appli Sequence 13, Appli Sequence 11, Appli Sequence 11, Appli Sequence 15, Appli Sequence 2, Appli Sequence 2, Appli Sequence 365, Appli Sequence 365, Appli Sequence 365, Appli Sequence 365, Appli Appli Appli Appli Sequence 1, A Sequence 1, A Sequence 3, A Description 1 US-09-970-944-1 3 US-09-918-779-1 7 US-10-624-932-1 7 US-10-933-261-1 5 US-10-240-154-15 6 US-09-933-261-2 5 US-10-240-154-15 6 US-09-933-261-2 5 US-10-296-115-365 1 US-09-833-311-1806 3 US-10-296-115-365 SUMMARIES 113 113 113 113 113 Query Match Length 1282 2860 2860 2860 2752 2752 3580 2697 1787 1787 Score 2881 2676.4 2676.4 22035.8 2235.8 2235.8 2235.8 11570.4 11570.4 11193.6 889 889 887.4 Result

Sequence 3, Appli	· LC	Semience 55. April	3.7	8	Sequence 14	14	145	145	145,	145,	145,	a 145,	equence 145.	145	equence 145.	equence 145.	equence 145.	145	equence 145,	145,	145,	145,	145,	145,	145,	145	145	145	145,	equence 1
US-10-218-779-	US-09-972-211-5	3 US-10-096-	3 US-10-037-417-3	US-09-816-828-18	3 US-10-147-493-14	3 US-10-145-127-1	3 US-10-160-503-14	US-10-143-118-14	US-10-144-993-14	US-10-158-787-14	US-10-140-024-14	US-10-140-808-14	US-10-152-405-14	US-10-127-852A-14	US-10-127-9	US-10-128-685A-14	US-10-131-820A-14	US-10-142-886-145	US-10-146-728-14	US-10-146-786-14	US-10-147-499-14	US-10-157-798-14	US-10-028-072-14	US-10-121-049-14	US-10-123-904-14	US-10-140-470-14	US-10-175-746-14	US-10-176-918-14	-10-176-921-1	US-10-137-865-14
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## ALIGNMENTS

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Sequence 1, Application US/08970944

Publication No. US20030204052A1

Publication No. US20030204052A1

Publication No. US20030204052A1

APPLICANT: Rastelli, Luca

APPLICANT: Rastelli, Luca

APPLICANT: Rastelli, Luca

APPLICANT: Sinkets, Richard A

TITLE OF INVENTION: Antibodies Directed Against these Proteins

TITLE OF INVENTION: Antibodies Directed Against these Proteins

CURRENT FILING DATE: 2002-05-02

PRIOR APPLICATION NUMBER: 60/237,862

PRIOR PAPLICATION NUMBER: 60/237,862

PRIOR PELING DATE: 2000-10-04

NUMBER OF SEQ ID NOS: 62

SOFTWARE: PatentIn Ver: 2.1

SEQ ID NO 1

LENGTH: 2881
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100.0%; Pred. No. 0;
tive 0; Mismatches
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Matches 2881; Conservative
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ORGANISM: Homo sapiens
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98.9%; Pred. No. 0;
iive 0; Mismatches 21; Indels
PRIOR APPLICATION NUMBER: 60/223,752
PRIOR PLILING DATE: 2000-08-08
PRIOR PLILING DATE: 2000-08-08
PRIOR PLILING DATE: 2000-08-08
PRIOR APPLICATION NUMBER: 60/223,770
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                                                                                                                       342 GACCACGIGATCGAGCGCAGCACGGGAGCAGTGGTGAGCCGACCATGGAGGTCCGC
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                                                                                                                                                                                                                           TGCGTGGCATGGAGCTCCTCGGGCACCACCAAGAGTCAGAAGGCCTACATCGCCATAGCC
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APPLICANT: Groses, William
APPLICANT: Lepley, Denise
APPLICANT: Lepley, Denise
APPLICANT: Burgess, Catherine
APPLICANT: Burgess, Catherine
APPLICANT: Brigess, Catherine
APPLICANT: Bloomail, John
APPLICANT: Smithson, Glennda
TITLE OF INVENTION: Order Broteins and Nucleic Acids Encoding Same
TILE REFERENCE: 21402-074 US
CURRENT FAPLICATION NUMBER: 09/918,779
PRIOR FILING DATE: 2000-03-07-21
PRIOR APPLICATION NUMBER: 60/221,409
PRIOR PLILING DATE: 2000-08-04
PRIOR PLILING DATE: 2000-08-08
PRIOR PLILORION NUMBER: 60/223,769
PRIOR PLILORION NUMBER: 60/225,470
PRIOR PLILORION NUMBER: 60/225,470
PRIOR PLILING DATE: 2000-08-15
PRIOR PLILING DATE: 2000-08-15
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PRIOR PLILOR DATE: 2000-08-15
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Pred. No. 0;
0; Mismatches
Sequence 1, Application US/10624932
Publication No. US20040096877A1
GENERAL INFORMATION:
                                                   APPLICANT: Taupier, Raymond
APPLICANT: Padigaru, Muralidhara
APPLICANT: Rastelli, Luca
APPLICANT: Spaderna, Steven
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98.9%;
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Spytek, Kimberly
Shenoy, Suresh
                                                                                                                                                                                                           Li, Li
Gusev, Vladimir
Grosse, William
Alsobrook, John
Lepley, Denise
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Best Local Similarity 98.9
Matches 2728; Conservative
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CORGANISM: Homo sapiens
US-10-624-932-1
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Qy         2439         AAGGACACAAGGTTTGCTGAGCTGGCTCTGAGAGTGAAGCGGGGCTCCCAGCCCTG         2499           Db         2395         AAGGACCACAAGGTTTGCTGAGCTGCTGCTCTCTCTCTCAGCCTG         2454           Qy         2499         GTGGCCCCAGTGCTTCAAGATCCCTTCTCTCTATCGGCAGAAGATAATTTCCAGCCTG         2455           GTGGCCCCAGTGCTTCAAGATCCCCTTCTCTCTTTCGGCAGAAGATAATTTCCAGCCTG         2514           Qy         2559         GACCCACTGTGAGGCGGGTGCCCTTCCTCATTCGGCAGAAGATAATTTCCAGCCTG         2514           Qy         2559         GACCCACTGTAGGCGGGTGCCGACTGGCGGACTCTGGCCCAGAAGATAATTTCCAGCCTG         2514           Qy         2619         AGCCATCTTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAAAATTTCCAGCCTGGACTGTGGCTGGC	NESULT 4  US-10-311-523-13  Sequence 13, Application US/10311623  Publication No. US200400232441  JERERAL INCREMATION: APPLICANT: INCTE GENOMICS, INC.; GRIFFIN, Jennifer A. APPLICANT: TANG, T. TOM; LAM, T. TRIGOULEY, Catherine M. APPLICANT: TANG, Y. TOM; LAM, Preetid APPLICANT: PANG, Y. TOM; LAM, Preetid APPLICANT: POLICKY, Jennifer L.; AZIWZAI, Yalda APPLICANT: PANG, Monique G.; BURCORD, Meil APPLICANT: PANGHAN, Olga, ARVIZU, Chandra S. APPLICANT: BANDAM, Olga, ARVIZU, Chandra S. APPLICANT: PANGHAN, Olga, ARVIZU, Chandra S. APPLICANT: WAG, JUHMAN, B. WAGHANMALA, Wadhusudan M. APPLICANT: UNGS. RECEPTORS ITILE OF INVENTION RECEPTORS FILE REFERENCE: PP-0793 US CURRENT PELLOR DATE: 2002-12-17 PRIOR PELLOR DATE: 2002-12-17 PRIOR APPLICATION NUMBER: US 60/214, 027 PRIOR APPLICATION NUMBER: US 60/214, 027 PRIOR PELLOR DATE: 2000-06-21 PRIOR PELCOR DATE: 2000-06-21 PRIOR PELCOR DATE: 2000-06-21 PRIOR PERCENTE: PRECEDENCE PERCENTER THEORYATION: LACYTE ID NO. US20040023244A1 6052371CB1 OTHER THEORYATION: LACYTE ID NO. US20040023244A1 6052371CB1	US-10-311-623-13  Query Match  Query Match  Best Local Similarity 93.4%; Score 2402.6; DB 17; Length 3580;  Best Local Similarity 93.4%; Pred. No. 0;  Matches 2615; Conservative 0; Mismatches 9; Indels 177; Gaps 3;  Qy 84 GCCATGGCCCGGCCTGTGGCCAGCGTCCTGGGCATAGTCCTCGCCGCTTGG 143
1362   GACCTCAGCACCACCACCACCACCAGGGCAGCTCTCTCTCCCCGGCAGGATGGGCCC   1418		9 TTGCACTGCACCTTCACCCTGGAGCGTGTCAGCCCCAGCACTGGTGACCTGGCCTGCAAG

1224 CTCATCCTCGTTANTTCCCCGAAGAAGAGGGCTGGAATCAAATGGCTGACTCGTC   1283	CTCAGGAGGAGGAGACTGAGAGAGCGGCCTATCCATTTTATCAGGAGCCAGG 192 GTCCTGCACTTCAAGGACAGTTACCACAAGCTGGGGGGACAGCTGATCCAGGAGCCACGG 192 GTCCTGCACTTCAAGGACAGTTACCACAACCTGGGCCTATCCATCC
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                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                     312;
                                                                                                                                                                                                        Score 2235.8;
Pred. No. 0;
                                                                                                                                                                                                                                       0; Mismatches
             UC96-217
                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: CDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
REGISTRATION NUMBER: 36,627
          REFERENCE/DOCKET NUMBER: 1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                              LENGTH: 3014 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                           77.6%;
88.5%;
                                                                                                                                                                                                                          Best Local Similarity 88.5
Matches 2474; Conservative
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COMPUTER: IBM PC compatible
ODERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/933,261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kazuko, Keino-Masu
TITLE OF INVENTION: Netrin Receptors
NUMBER OF SEQUENCES: B
CORRESPONDENCE ADDRESS:
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FILING DATE: «UNKNOWN»
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Leonardo, E. David
Hink, Lindsay
Macuk, E. Masayuki
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CLASSIFICATION: <Unknown>
APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/09933261
Publication No. US20030040046A1
GENERAL INFORMATION:
APPLICANT: Tessier-Lavigne,
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COMPUTER READABLE FORM:
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Pred. No. 0;
0; Mismatches 312; Indels
                                                                                                                                                                                                                                                                                        Version #1.30
                          CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STRET: 268 BUSH STREET, SUITE 3200
STRET: CALIFORNIA
COUNTRY: USA
                                                                                                                                                                   ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Vei
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/256,702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: UC96-217
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
                                                                                                                                                                                                                                                                                                                                                                                                    RAPPLICATION DATA:
PAPELICATION NUMBER: US/09/933,261
FILING DATE: 20-Aug-2001
APPLICATION NUMBER: 08/808,982
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) SEQUENCE DESCRIPTION: SEQ ID NO:
US-10-256-702-1
                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 27-Sep-2002 CLASSIFICATION: <Unknown>
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STRANDEDNESS: double
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CHARACTERISTICS:
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ilarity 88.5%;
Conservative
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Best Local Simi
Matches 2474;
              NUMBER
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                                                                                             2695 TGAGACCAGCCAGGCGGTAATGCCTACATCTCACCAGCTTTGACACCTGCCAGGGACA
                                                                      TGAGGCCGGCCAGGCCCG--ACACCTACACTCTCACCAGCTTTGGCACCCACCCAAGGACA
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Pred. No. 0;
0; Mismatches 291; Indels
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USACULO-240-154-15

Sequence 15, Application US/10240154

PUBLication No. US20030175741A1

SEGUERAL INFORMATION: APPLICANT: Cochran et al.

TITLE OF INVENTION: SCHIZOPHRENIA RELATED GEI

FILE REFERENCE: CKFW-P01-006

CURRENT FILING DATE: 2001-04-02

PRIOR APPLICATION NUMBER: US/10/240,154

CURRENT FILING DATE: 2001-04-02

NUMBER OF SEQ ID NOS: 34

SOFTWARE: Patentin version 3.2

LENGTH: 2697
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Best Local Similarity 88.9%;
Matches 2403; Conservative
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ORGANISM: Rattus
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g g	687 ACGCGGGGGCACACCTGGTGGTGCGACAGGCCCGCCTTGCTGCCCGGCCGACACGCCGGCGGGGGGGG	요 &	1678 AGCTIGTIGGGCCCCCCAGGAGTCCTGCTCACCCGGCCAGTCATCCTTGCAATGGACCACTGT 1737 1824 GGGGAGCCCGGCCTGACAGCTGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGGCAGC 1883
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9 y	TCCTG 125	<i>&amp;</i> &	2424 AACTICAACAICAAGAACACAAGGITIGCIGAGCIGCTGGCTCTGGAGAGTGAAGGG 2483
da yo	1258 CTCACCATCCAGCCAGACCTCAGCACCACTACCACCTACCAGGGCAGTCTATGTTCG 1317 1404 CGGCAGGATGGGCCCAAGCTCCAAGTTCAACTCAATGGCACTGAGCCCCTG 1463	که ط	2484 GGGGTCCCAGCCCTGGTGGGCCCCCAGTGCCTTCAAGATCCCCTTCCTCATTCGGCAGAAG 2543 2395 GAGTTCCCAGCCCTGGTGGGCCCCAGTGCCTTCAAGATCCCCTTCTCATTCGGCAAAAG 2454
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à i	1524 TCCCGCCTCTCCACAGAACTACTTCCGCTCCCTGCCCCGAGGCACCAGCAACATGACC 1583	À q	515 AAACTICACCTGGACAGCCATCTTAGCTTCTTTGCCTCCAAGCCCAGCCCTACAGCCATG
g Zo	TATGGGACTICCAACTCCTCGGGGGCCGGCTGATGATCCCTAATACAGGTATCAGCTC 16	Qy	2664 AICCICAACCIGGGAGGGGGGCACITCCCCAACGGCAACCICAGCCAGCIGGCIGGA 2723
da ya	1498 TACGGGACCTTCAACTTCCTCGGGGGCCGGCTGATGATCCCTAATACGGGGATCACCTC 1557 1644 CTCATCCCCCGAGATGCCATACCCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCAC 1703	% qq	2724 GCAGTGGCTGGACTGGGCCAGCCAGCCTGGCTTTCACAGTGTCGGAGGCTGAGTGC 2783 2635 GCTGTGGCCGGACTGGGCCAACCAGATGCTGGCCTCTTCACGGTGTCGGAGGCCGAGTGT 2694

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                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/933,261
FILING DATE: 20-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                               ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP STREET: 268 BUSH STREET, SUITE 3200 CITY: SAN FRANCISCO STATE: CALIFORNIA COUNTRY: USA
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Pred. No. 0;
0; Mismatches
                                                                                                                                                 APPLICANT: Tessier-Lavigne, Marc
Leonardo, E. David
Hink, Lindsay
Masu, Masayuki
Kazuko, Keino-Masu
TITLE OF INVENTION: Netrin Receptors
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 08/808,982
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MOLECULE TYPE: CDNA
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
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:15) 343-4342
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TELECOMMUNICATION INFORMATION:
                                                                      RESULT 8
US-09-933-261-2
'Sequence 2, Application US/09933261
'Publication No. US20030040046A1
'GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid_
STRANDEDNESS: double
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96.9%;
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Best Local Similarity 96.9
Matches 1721, Conservative
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                                                                                                                                                                      Score 1570.4;
Pred. No. 0;
                                                                                                                                                                                                        0; Mismatches
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1787 base pairs
TYPF: nucleic acid
STRANDEDNESS: double
TOPPLOGY: linear
MOLECULE TYPE: CDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                        54.5%;
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Matches 1721; Conservative
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                          CCAGCCCTGGTGGCCCCAGTGCCTTCAAGATCCCCTTTCCTCATTCGGCAGAAGATAATT
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/256,702
FILING DATE: 27-Sep-2002
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
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REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: UC96-217
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/09/933,261
FILING DATE: 20-Aug-2001
APPLICATION NUMBER: 08/808,982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kazuko, Keino-Masu
TITLE OF INVENTION: Netrin Receptors
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
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E. David
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US-10-256-702-2
; Sequence 2, Application US/10256702
; Publication No. US20030059859A1
; GENERAL INFORMATION:
; APPLICANT: Tessier-Lavigne, I
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Hink, Lindsay
Masu, Masayuki
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PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: US09/552,317
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 1478
SEQ ID NO 365
LENGTH: 1321
TYPE: DNA
                                                                                          Query Match 41.4%;
Best Local Similarity 97.8%;
Matches 1295; Conservative
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                                                                ; ORGANISM: Homo
US-10-296-115-365
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                                          TCCCTCGAGTACAACATCCGGGTCTACTGCCTGCATGAACACCCACGATGCACTCAAGGAG
                                                                                       TTCAAGGACAGTTACCACAACCTGCGCCTATCCATCCACGATGTGCCCCAGCTCCCTGTGG
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Publication No. US20040053248A1
GENERAL INFORMATION:
APPLICANT: Hyseq Inc
ITLE OF INVENTION: No. US20040053248A1e1 Nuc
FILE REFERENCE: 784PCT
CURRENT FILING DATE: 2002-11-18
PRIOR APPLICATION NUMBER: US/10/296,115
PRIOR APPLICATION NUMBER: US/9/488,725
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US-10-296-115-365
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Patent No. US20020132090A1
GENERAL INFORMATION:
TITLE OF INVENTION: No. US20020132090A1e1 Nuc
FILE REPERENCE: 8000-119
CURRENT APPLICATION NUMBER: US/09/833,381
CURRENT FILING DATE: 2001-04-11
PRIOR FILING DATE: 2001-06-21
PRIOR FILING DATE: 2000-02-29
NUMBER OF SEQ ID NOS: 2050
SOFTWARE: FastSEQ for Windows Version 3.0
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 1282
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ORGANISM: Homo sapiens
FRATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(1282)
OTHER INFORMATION: n = A
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APPLICANT: Sethusen, Bryan D.
APPLICANT: Malyankar, Uriel M.
APPLICANT: Gangolli, Esha A.
APPLICANT: Gangolli, Esha A.
TITLE OF INVENTURE SOUS.
FILE REPERENCE: 21402-114 CIP
CURRENT FILING DATE: 2003-03-10
PRIOR PLICATION NUMBER: 05/25,934
PRIOR PLICATION NUMBER: 60/255,936
PRIOR PLICATION NUMBER: 60/255,926
PRIOR PLICATION NUMBER: 60/256,180
PRIOR PLICATION NUMBER: 60/264,180
PRIOR PLICATION NUMBER: 60/264,180
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Pred. No. 2.1e-211;
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2765 AGIGICGGAGGCIGAGIGCIGAGGCCGG
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                                                                                                                                                                                                                          ' Sequence 1, Application US/10087684
' Publication No. US20040029116A1
' GENERAL INFORMATION:
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Padigaru, Muralidhara
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Shenoy, Suresh G.
Rastelli, Luca
Tchernev, Velizar T.
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Best Local Similarity 60.7%;
Matches 1637; Conservative (
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Query Match
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Rieger, Daniel K.
Burgess, Cathereine E.
Casman, Stacie, J.
Spytek, Kimberly A.
Boldog, Ferenc L.
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Padigaru, Muralidhara
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Tchernev, Velizar T
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Stone, David J.
Grosse, William M.
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Shenoy, Suresh G.
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Vernet, Corine A.M. Zerhusen, Bryan D. Malyankar, Uriel M.

APPLICANT: APPLICANT: APPLICANT:

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APPLICANT: Miller, Charles B.
APPLICANT: Miller, Charles B.
APPLICANT: Miller, Charles B.
APPLICANT: Miller, Charles B.
APPLICANT: Gangolli, Esha A.
ITLE OF INVENTION: PROTEINS AND NUCLEIC ACIDS ENCODING SAME FILE EPERENCE: 2140-2-14 CIP
CURRENT APPLICATION NUMBER: US/10/087,684
CURRENT APPLICATION NUMBER: US/10/087,684
PRIOR FILING DATE: 2000-11-29
PRIOR FILING DATE: 2000-11-29
PRIOR FILING DATE: 2000-11-30
PRIOR FILING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-03-08
PRIOR FILING DATE: 2001-03-08
PRIOR FILING DATE: 2001-08-06
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Pred. No. 5.4e-211;
0; Mismatches 961;
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Conservative
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SOFTWARE: CuraSeqList veri
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LOCATION: (59)..(2857)
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APPLICANT: Gangolli, Esha
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REPERENCE: 1402-214
CURRENT APPLICATION NUMBER: US/10/218,779
CURRENT FILING DATE: 2002-08-14
PRIOR PELICATION NUMBER: 60/253,834
PRIOR FILING DATE: 2000-11-29
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Pred. No. 5.4e-211;
0; Mismatches 961;
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PRIOR FILING DATE: 2000-11-30
PRIOR FILING DATE: 2000-11-30
PRIOR FILING DATE: 2001-01-25
PRIOR FILING DATE: 2001-01-25
PRIOR FILING DATE: 2001-08-20
PRIOR FILING DATE: 2001-08-20
PRIOR FILING DATE: 2001-10-05
NUMBER OF SEQ ID NOS: 216
SOFTWARE: Patentin Ver. 2.1
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Mishra, Vishnu
Patturajan, Meera
Shenoy, Suresh
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Lepley, Denise
Rieger, Daniel
Burgess, Catherine
Casman, Stacie
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Best Local Similarity 60.6%;
Matches 1636; Conservative
                                                                                                                      Ellerman, Karen
Stone, David
Gerlach, Valerie
Grosse, William
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Tchernev, Velizar
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Malyankar, Uriel
Guo, Xiaojia
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Millet, Isabelle
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                      Edinger, Shlomit
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Boldog, Ferenc
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AY411749 Mus muscu
BX364574 BX364574
BC033727 Homo sapi
B1618609 603033362
BX345407 BX345406
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BX422753 BX422753
BQ691915 AGRCOURT
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BQ689148 AGENCOURT
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Homo sapiens UNC5C gene, VIRTUAL TRANSCRIPT, partial sequence,
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(bases 1 to 2008).

Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, W. Winte, T.J., Sninsky, J.J., Inferring nonneutral evolution from human-chimp-mouse orthologous
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Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
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Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA.
This sequence was made by sequencing genomic exons and ordering them based on alignment.
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                                                                                                                                                                                                                                                                                                                                         DB 29;
                                                                                                                                                                                                                                                                                                                                 Score 907.8; DB 29;
Pred. No. 3.9e-142;
0; Mismatches 1014;
                                                                                         Location/Qualifiers
1. 2802
/ Organism="Homo sapiens"
// Organism="Homo sapiens"
// Lype="genomic DNA"
// Locas="taxon:9606"
// Gene="UNOSC"
/locus_tag="HCM2575"
                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 60.3%;
Matches 1660; Conservative
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                                                                                                       Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
Direct Submitsion
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              190 TGCCTGGTGCCAACCCGGACCTGCTTCCCCAGTGGGAGCCCGAGGATGTGTACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TICCATCTGACCCACTGCCACTTGCCACTTCCTCATTGAGCCCGAGGAAGCTTACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   338 AAACCTCTGGTCTAATTGTGAGAGAAGTGAGCATTGAGGATTTCACGCCAGCAGGTGGAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 29; Length 2791;
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              Adams,M.D. and Cargill,M.
Inferring nonneutral evolution from human-chimp-mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31.2%; Score 898.6; DB 29; llarity 61.5%; Pred. No. 1.4e-140; Conservative 0; Mismatches 939;
                                                                    Science 302 (5652), 1960-1963 (2003)
14671302
                                                                                                                                                                                                                                                                                                                             1. .2791
/organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                    /mol_type="genomic DNA
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="UNC5C"
/locus_tag="HCM2575"
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Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
TGCCTGCTACGTCTTCACCGAGCAGCTGGGCCGCTTTGCCCTGGTGGGAGAGGCCCTCAG
                                                                                                     2151 ACATCTTGAGAGAGAGGAGGAGGACTCCTAGAAGAACCTAAGGCTCTTTTAA
                                                                                                                                                                                                                                                                                                             2195 GGACAGTIACCACAACCIGCGCCTAICCAICCACGAIGIGCCCCAGCICCCTGIGGAAGAG
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                                                                                                                                                                                2135 GCAGCTGGAGAAGCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCCTGCACTTCAA
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                                                                            CGTGGCTGCCGCCAAGCGCCTCAAGCTGCTTTGCGCCGGGGGCCTGCACCTCCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGACAGCCATCTCAGCTTCTTTGCCTCCAAGCCCAGGCCCACAGCCATGATCCTCAACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2675 GIGGGAGGCGCGCACTICCCCAACGCCAACCTCAGCCAGCTGCAGCAGCAGTGGCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCTGGACCCACCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAAGAAACTCCACCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2691 TTGGGAAGCACAGAACTTCCCAGATGGAAACCTGAGCATGCTGGCAGCTGTTGGAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2791 bp DNA linear GSS 15-DEC VIRTUAL TRANSCRIPT, partial sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AATGGGAAGACATGAAACGGTGGTGTCCTTAGCAGCAGAAGGGCAGTATTAA 2802
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GSS.
Mus musculus (house mouse)
Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus UNC5C gene,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             genomic survey sequence. AY406493
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1916   CASTOCACCACACACACACACACACACACACACACACACACAC	RESULT 3  AK031655  LOCUS  LOCUS  MINIMA linear HTC 18-SEP-2003  LOCUS  DEFINITION Mus musculus 13 days embryo male testis CDNA, RIKEN full-length enriched library, clone:6030473424 product:unc5 homolog (C. elegans) 3, full insert sequence.  ACCESSION AK031655  AK031655.1 GI:26327502  KEYWORDS  HTC; CAP trapper.
910 TOTATA CAGGACCACATCA CARANA CAGACCACA CAGGACCA CACCA CAGACCA ACCAS A	

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REFERENCE AUTHORS JOURNAL MEDLINE

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/translation="MRKGLRATRARCGLGIGYLLQMLVLPALALLSASGTGSRAQDDB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ILTLHHCADPSTEDWKIQLKNQAVQGQWEDVVVVGEERRTTPCYIQLDAEACHLITEN
LSTYALVQGSTTKAAAKRLKIAIFGFLCCSSLEYSIRVYCLDDTQDALKEVLQLERQW
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GPSAFSIPLPIRQKLCSSLDAPQTRGHDWRMLAHKLNLDRYLNYFAIKSSPTGYILDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SGVSLLIPAGAI PQGRVYEMYVTVHRKENMRPPMEDSQTLLTPVVSCGPPGALLTRPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    455 AAACCTCTGGTCTAATTGTGAGAGAAGTGAGCATTGAGATTTCACGCCAGCAGGTGGAGG 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  190 TGCCTGGTGCCAACCCGGACCTGCTTCCCCACTTCCTGGTGGAGCCCGAGGATGTGTACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   310 TCAAGTGCAACGGGGAGTGGGTGCGCCAGGTGGACCACGTGATCGAGCGCAGCACAGACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCAAGTGCAACAGCGAGTGGGTTCATCAGAAGGACCACGTAGTAGACGAGAGGAGTAGATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  275 TICCAICTGACCCACCIGAGCCATIGCCACACTICCTCATIGAGCCCGAGGAAGCTIACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                250 ICGICAAGAACAAGCCAGIGCIGCIIGIGIGCAAGGCCGIGCCCGCCACGCAGGAICIICI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 335 Tréricaadaacaaccréréaaccrerarreraadeccaeccreccadecadereracr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     635 ccricegaaadegaacierrecaecaecaeaacrerracrecaererecececeae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     695 GGATCCCAGTGGCTGAGGTAGATGGCTAAAGAATGAGACATAATTGATCCTGCTGAAG
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                                                                                                                                                                                                                                                                                                                                                                                                               /note="unnamed protein product; putative unc5 homolog (C. elegans) 3 (MGD MGI:1095412, GB LM 009472, evidence: BLASTN, 99%; match=464) " (codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 871.6; DB 11; Length 3790;
Pred. No. 5.5e-136;
0; Mismatches 944; Indels 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WEAQNFPDGNLSMLAAVLEEMGRHETVVYLAAEGQY
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/strain="C57BL/6J"
/db_xref="FaNTOM DB:6030473H24"
/db_xref="MGI:2394911"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="BAC27495.1"
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                    organism="Mus musculus"
                                                                                                                                                                               /db_xref="taxon:10090"
/clone="6030473H24"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30.3%;
                                                                                                                                                                                                                                                       sex="male"
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Matches 1641; Conservative
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                                                                                                                                                                                                                                                                                                                                                    Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Komo, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumin, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, R., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Yoneda, Y., Isawa, M., Ohara, B., Matahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Riki, Y., Muramatsu, M., Inouce, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system-384-format Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Pukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatuu, N., Hiramoto, K., Hiracoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Nakamura, M., Nishi, K., Nomura, K., Karoh, H., Kohno, H., Koduda, M., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Takada, Y., Taqami, M., Taqawa, A., Takahashi, F., Takahushi, T., Takaku-Akahira, S., Muramatsu, M., and Hayashizaki, Y., Toya, T., Yasumishi, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 565-573 (2002)
6 (bases 1 to 3790)
                                                                 Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yokohama,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Research Group in Riken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Rike Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The FANTOM Consortium and the RIKEN Genome Exploration Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Teurumi-ku, Yokoham Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Please visit our web site for further details.
                                                                                                                               caininci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/
Location/Qualifiers
1. .3790
                                                          Chordata;
Rodentia;
musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           prepare mouse tissues.
                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
                        musculus
                                                                                                                                                                                                                                                                                             10349636
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JOURNAL REFERENCE

TITLE

AUTHORS

AUTHORS

REFERENCE AUTHORS

JOURNAL

TITLE

TITLE JOURNAL

COMMENT

JOURNAL MEDLINE

TITLE

PUBMED REFERENCE 8 249

Gaps

334 309 429

489

634

754

Source

FEATURES

670 ACCCCAATGTATA	ACCCCAATGTATACATCACGCGGGAGCACAGCCTGGTGGTGCGACAGGCCCGGCCTTGCTG 729	qq	1826
755 Arcggaactita		ŏ	169
	ACACGCCAACTACACCTGCGTGGCCAAGAACATCGTGGCACGTCGCCGCAGCGCTCCG 789	qa	188(
815 ATACAGCAAATTA		ζŏ	175
		qq	194
875 CCACTGTCATCGT		λō	181
	GCGCCAGCTGTGGGCGCGGCTGGCAGAAACGGAGCTGCACCACCACCCGGGCCTC 909	qu	200
		δ	187
910 TCAACGGGGGCGC	TCAACGGGGGCCTTTCTGTGAGGGCCAGAATGTCCATGACCGCACCGTCTCTCTC	qq	206
		ζŏ	193
-	TIGICICTOTOGACCGCAGCTGGAGCCCGTGGAGCAAGTGGTCGGCCTGTGGGGCTTGGACTTGCAACTTGC	qq	212
		ζ	199
	GCACCCCACTGGCGGAGCCGTCAGGTCTCTGACCCAGCACCCAGGGGGGGG	qa	218
		ζŏ	205
	GCCAGGCACTGACCTGGACACCCGCAACTGTACCAGTGACCTCTGACAACAGAGGACACAACAGGAACAACAGGAACAACAACA	qa	224
		λ	211
	1001	qa	230
		ζö	217
	GCCCTGAGGACGTGGCCCTCTATGTGGGCCTCATCGCCGTGGCCGTCTCCCTGGTCC 1209	q <sub>Q</sub>	236
1292 ACTCAGATGATGI		ò	223
		Ωp	242
1352 TCACTGTTGTGG		δλ	229
	TGGCTGACTCGTCGATTCTCCACCCTCAGCCCTCAGCCATCAGCCCAGCAAG 1329	qq	248
1412 TCATTGACTCCTC		٥y	235
	AGCCGGACCTCAGCACCACCACCACCATCAGG	qq	254
		ò	241
		qq	260
w		δŏ	247
	GCACCTGCTCAGCCCCCTGGGTGGCGGCCGCCACACTGCACCACGTCTCCCACCTC 1504	qq	266
		ò	253
	rgaggccgaggagttcgrccccccccccccc	qu	272
		ζŏ	259
		අු	278
vo	AGAATGAGGCCCTTAACCTGAAGAACCAGAGCCTCGCAAGACAGAC	ζō	265
	TGACCTATGGGACCTTCAACTTCCTCGGGGGCGGGCTGATGATCCCTAATACAGGTACA 1638	qc	284
1766 CAGCATTIGGIA	CAGCATTIGGIACCTICAACICICTIGGGGGGGGGGGGGG	δλ	271

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VERSION

SOURCE

TITLE

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/ LEARS LALL OF HYRARGYRSALLLALLCWDPTPSLAGYDSAGGYLPDSYPSAPA
/ LEARS LALL OF HYRARGYRSALLLALLLCWDPTPSLAGYDSAGGYLPDSYPSAPA
BOLPYFLLEPQDAYIYKNKRVELHCRAFPATQIYFKCNGEWYSQNDHYTQESLIDEATG
LRYBEVQIEVSKRQYVEELFGLEDYWQCYARASSGTTFKSRRAYITATATKNENDOEPL
AKBYPLDHEYLLCCRPPEGYVAEVBWLKNEDYIDPAQDTNFLLTIDHNLIIRQARLS
DTANYTCVAKNIVAKRRSTAATVIVYVNGGWSSWAEMSPCSNECGRGWQKRTFTCTNP
APLAGGAFCEGGAPRCTACTTVCPVDGAWTEWSKWASACSTECAHWRSRECMAPPONG
GRCSGTLLDSKNCTDGLCVLNQRTLNDPKSHPLETSGDYALYAGLVAVFVVAVANG
ARGVIVYRRNCRDPDTDITDSSAALTGGFHPWNFKTARPNNPQLLHPSAPPDLTASAG
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CAEVIAGDWIPQLAYRARSTLESSGSTVLLSPVALKESVLELLCGYLVF
PRESTANGENT PROLICESTENSCHTLDGGGSTVF
PRESTANGENT PROLICESTENSCHTLDGGGSTVF
PRESTANGENT PROLICESTENSCHTLNDGGSTVF
PRESTANGENT PROLICESTENSCHTLLDGGGSTVF
PRESTANGENT PROLICESTENSCHTLLDGGGSTVF
                                                                                                                                                                                                                                                       Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, URL:http://genome.gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp, Fax:81-45-503-9216)
Plax:81-45-503-9216)
Please visit our web site (http://genome.gsc.riken.go.jp/) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="medulla oblongata"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EPKDLLFKDSYHNLRLSLHDIPHAHWRSKLLAKYQEIPPYHYWNGSORALHCTFTLER
RISAGTEFTCKVRQVEREGOIFQLHTTLAETPAGSLDALCSAPGRAITTDJGSPYAF
KIPLSIROKT CSSLDAPDSRGNDWRLLAQKLSMDRYLNYFATKASPTGVILDIWEARQ
QDDGDLNSLASALEEMGKSEMLVAMATDGDC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="unnamed protein product; TRANSWEMBRANE RECEPTOR
UNC5H2 homolog [Rattus norvegicus] (SPTR|008722, evidence:
FASTY, 96.5%ID, 100%length, match=2835)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         540 GCCCTGCGGAGCAGCTGCCGTACTTCCTATTGGAGCCACAGGACGCCTACATCGTAAAG 599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     258 AACAAGCCAGTGCTTGTTGTGTGCCAAGGCCGTGCCGCCACGCAGATCTTCTTCAAGTGC 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                198 GCCAACCCGGACCTGCTTCCCCACTTCCTGGTGGAGCCCCGAGGATGTGTACATCGTCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28.4%; Score 818.4; DB 11; Length 3866; 59.6%; Pred. No. 4.9e-127; ive 0; Mismatches 961; Indels 138; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 db_xref="FANTOM_DB:6330415E02"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /protein_id="BAB31108.1"
/db_xref="GI:12857776"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="MGI:1910526"
/db_xref="taxon:10090"
/clone="6330415E02"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
1. .3866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   end: BamHI. Host: DH10B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    codon start=1
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                                                                                                                                                                                                                                    further details.
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                                                                                                                                                                                                    COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome_Res. 10 (10), 1617-1630 (2000)
2903 CAGCCGTCCTGGAAGAAATGGGAAGACATGAGACAGTGGTGTACTTGGCAGCAGAAGGAC 2962
                                                                                                                                                                                                                                                                                      HTC 20-SEP-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H., Arakwa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y., Arakwa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y., Harakwa, T., Bono, H., Hara, A., Hayatsu, N., Hiramoto, K., Isaku, Y., Kasukawa, T., Hori, F., Imotani, K., Ishi, Y., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Salto, H., Salto, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shibata, Y., Shinagawa, A., Sakai, F., Tanaka, T., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Yoshino, M., Muramatsu, M. and Hayashizaki, Y., Yoshida, K., Direct Submission

Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Yoneda, Y., Ishikawa, T., Ozawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inohe, Y., Kira, A. and Hayashizaki, Y. Okazaki, Y., Mutegraeted sequence analysis (RISA) system-384-format Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)

6 (bases 1 to 3866)
                                                                                                                                                                                                                                                                             AKON8177

3866 bp mRNA linear HTC 20-SEP-20C
Mus musculus adult male medulla oblongata cDNA, RIKBN full-length
enriched library, clone:633041502 product.TRANSMEMBRANE RECEPTOR
UNCSH2 homolog [Rattus norvegicus], full insert sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The RIKEN Genome Exploration Research Group Phase II Team and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The FANTOM Consortium and the RIKEN Genome Exploration Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Meth. Enzymol. 303, 19-44 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Carninci, P. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                            AK018177.1 GI:12857775
HTC; CAP trapper.
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AK018177
LOCUS
DEFINITION
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600 AACAAGCCAGTGGAACTGCACTGCAGAGCCTTCCCTGCCACGCAGATCTACTTCAAGTGT	CTTCAAGTGT 659	
318 AACGGGGAGTGGGCCAGGTGGACCACGTGATCGAGGCGCAGCACAGACGGGAGCAGT 	CGGGAGCAGT 377 	
378 GGTGAGCCGACCATGGAGGTCCGCATTAATGTCTCAAGGCAGCAGCAGGTCGAGAAGGTGTTC	GAAGGIGITC 437 	
438 GGGCTGGAGGAATACTGGTGCCAGTGCGTGGCATGGAGCTCCTCGGGCACCACCACCAAGAGT 	CACCAAGAGT 497           TACCAAGAGT 839	
498 CAGAAGGCCTACATCGCATAGCCAGATTGCGCAAGAACTTCGAGCAGGAGCGCTGGCC	GCCGCTGGCC 557             GCCTCTGGCC 899	
558 AAGGAGGTGTCCCTGGAGCAGGGATCGTGCTGCCCTGCC	GGGCATCCCT 617                  GGGAGTGCCT 959	
618 CCAGCCGAGGTGGGTCCGGAACGAGGACCTGGTGGACCCGTCCCTGGACCCCAT	GGACCCCAAT 677            GGACACTAAC 1019	
678 GIATACAICACGCGGGAGCACCAGCCTGGTGGCGACACAGCCCGCCTTGCTGACACGCCCCCCCTGCTGACACGCCCCCAGGCGCGCCCTCTCAGACGCCCCAGGCGCGCGC	TGACAGGCC 737 	
738 AACTACACCTGGGTGGCCAAGAACATCGTGGCACGTGGCGCGCGC	:cgcrgcrgrc 797 	
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918 GGCGCTTTCTGTGAGGGCAGAATGTCCATGACCGCACCGTCTCTCTTCTGCTTGTTGTCTCT	rgcrrgrcrr 977 	
978 GTGGACGCAGCTGGAGCCCGTGGACCAGTCGCCCTGTGGGCTGGACTGCACCCAC	ACTGCACCCAC 1037 	
1038 IGGCGGAGCCGTGAGTGCTCTGACCCAGCACCCGCAACGGAGGGAG	AGTGCCAGGC 1097        CTGCAGCGG 1436	
1098 ACTGACCTGGACACCGCAACTGTACCAGTGACCTCTGTGTACACAGTGCTTCTGGCC	CTTCTGGCC 1155 AGAGAACTCTA 1496	
1156	ATGTGGGCCTC 1184 	
185	rcgrtrattgc 1241           rcgrataccg 1616	
242	TCACCTCAGGC 1298       TCACTGGTGGC 1676	
299	TCACC 1352 	

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Query Match         26.5%;         Score 763.2;         DB 29;         Length 2532;           Best Local Similarity         60.0%;         Pred. No. 7.6e-118;           Matches 1515;         Conservative         0;         Mismatches 873;         Indels 138;         Gaps           393         GAGGTCGCGATTAATGTCTTAAAGGTCGTCGGTCGAGAAGGTCTTCGGGCTGGAGGATAC	DB 73 TGGTGCCAGTGGCCTGGAGCTCCGCGGGCACCACCAAGAGTCGCCCAGCCTACGTC 132  QY 513 CGCATAGCCAAATTGCGCAAAACTTCCAGCAGAGCCTGGCCTAGGCCTACCTG 572  DB 133 CGCATCGCCTACCTGCGCAAGAACTTCGATCAGAGCCTCTGGGCAAGGTGCCCTTG 192  QY 573 GAGCAGGCATCGTGCTGCCCTGCGCTCCACCCGAGGGCATCCCTCCAGCCCAGCGAGGTGCCCTTG 192		753	93 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9
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December   December	RESULT 6  AV406492  LOCUS  LOCUS  LOCUS  AV406492  AV406492  AV406492  AV406492  LOCUS  RATIFICAN  RATERIANSCRIPT, Partial sequence,  AV406492.1 G1:39762466  SWEANNORD  SWEATHORD  AV406492.1 G1:39762466  SWEANNORD  AV406492.1 G1:39762466  SWEANNORD  AV406492.1 G1:39762466  SWEANNORD  AV406492.1 G1:39762466  SWEANNORD  RATERIANSCRIPT, Partial sequence,  AMMMALIA, Partial sequence,  AMMMALIA, Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferrieca, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,  Adams, M.D. and Cargill, M. White, T.J., Sninsky, J.J.,  PUBMED  AVATIANSCRIPTION NORMORENTAL Sequencing Genomic exons and ordering them based on alignment.  TITLE  Direct Submission Date (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  FEATURES  COMMENT  RESTREAMS  ROWALINE, MARS Made by Sequencing genomic exons and ordering them based on alignment.  FEATURES  LOCASION NORMORENT  RESTREAMS  AND
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/note="Organ: property of the start is a male brains, age range 23-27 yo. Library is oligo-dr
/note of the start is a male brain; New Stroyed upon cloning). Average insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 019. Note: this is a NIH_MGC Library."
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Pred. No. 7.5e-117;
0; Mismatches 88; Indels 16;
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(Dases 1 to 1034)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
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                                                        2211 AGGCAGCACCACAACCTGCGCCTGTCAATTCACGATATCGCCCATTCCCTCTGGAAGAG
                                                                                            TAAGCTCCTTGTCAGCTACCAGGAGATCCCCTTTTATCACATCTGGAATGGCACGCAGCG
                                                                                                                                 GTACTTGCACTGCACCTTCACCCTGGAGCGTGTCAGCCCCCAGCACTAGTGACCTGGCCTG
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Email: cgapbs-r@mail.nih.gov
Trissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC Clone distribution information car
found through the I.M.A.G.E. Consortium/Link at:
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High quality sequence stop: 793.
Location/Qualifiers
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/mol_type="mRNA"
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603029876F1 NIH_MGC_114 Homo
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BI758231.1 GI:15749809
EST.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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(Inpublished (2001)

(Contact: Genoscope

(Contact: Web: www.genoscope.cns.fr, Web: www.genoscope.cns.fr

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Pred. No. 7.9e-112;
4; Mismatches 7;
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/mol type="mRNA"
/db_xref="taxon:9606"
/clone="CSODC023YB10"
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Best Local Similarity 98.4%;
Matches 739; Conservative 4
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                                                                        AGATCTTCTTCAAGTGCAACGGGGAGTGGGTGCCCAGGTGGACCACGTGATCGAGCGCA 360
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Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
Soares, Ph.D. cDNA Library Arrayed by: Christa Prange, The
I.M.A.G.E. Consortium DNA Sequencing by: Washington University
Clone distribution: NCI-CGAP clone distribution information can k
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1125 Std Error: 0.00
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                AGATCTTCTTCAAGTGCAACGGGAGTGGGTGCGCCAGGTGGACCACGTGATCGAGCGCA
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High quality sequence stop: 446.
Location/Qualifiers
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COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Mod help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I M.A.G.E. Consortium (LINL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov/
Reb site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov/
Reb site: http://www.nisc.nih.gov/
Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
Blakesley, R.W., Bouffard, G.G., Reen, K., Wongta, J., Haghighi.P.,
Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Laric, P., Legaspi, R.,
Maduro, Q.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,
McDowell, J.D., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W.,
Tsurgeon, C., Vogt, J.L., Nanlaker, M.A., Wetherby, K.D., Wiggins, L.,
Young, A., Zhang, L.-H. and Green, E.D.
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Location/Qualifiers
                                                         HTC 19-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (02-JUL-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
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22388257
                                             BC033727
Homo sapiens netrin receptor Unc5h1, mRNA (cDNA clone IMACE:5166762), containing frame-shift errors.
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                                                                                                                                                                         BC033727.1 GI:21707230
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Strausberg, R.
                                                                                                                                                                                                                                   sapiens (human)
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/organism="Homo sapiens"

FEATURES

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Pred. No. 3.3e-109;
/mol type="mRNA"
/db_xref="taxon:9606"
/clone=InAdB:5166762"
/tissue_type="Brain, adult me
/clone_lib="NIH MGC_119"
/lab_host="DH10B"
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BX348193 Homo sapiens NEUROBLASTOMA COT 10-NORMALIZED Homo sapiens CDNA clone CSODB008YE02 5-PRIME, mRNA sequence.
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1. (bases 1 to 843)
11, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
                                                                                                                                                                                                                                                                     CCAGTGCTGCTTGTGTGCAAAGGCCGTGCCCGCCACGCAGATCTTCTAAGTGCAAACGGG
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BP 191 91006 EVRY cedex - France
Email: Seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This Sequence belongs to sequence cluster 3239.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSOBAF004ZD01_AF00293_L&cluster=3239.r.
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//lab_host="NB108"
//lab_host="NB108"
//lab_host="Organ: pooled brain, lung, testis; Vector:
pCMV-SPORTS; Sited 1: Not1; Site 2: EccRV (destroyed); RNA
Source anonymous pool of 6 male_brains, age range 23-27;
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (EccRV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH_MGC Library."
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B. (Asses I to 818)

S. NIH-MGC http://mgc.nci.nih.gov/.

I. Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov
Tissue Procurement: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CONA Library Preparation: Life Technologies, In
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larity 97.1%; Pred. No. 4e-109;
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/clone="IMAGE:5174559"
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BX345406.1 GI:30369001
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BP 191 91006 EVRY cedex - France
BEmail: segref@genoscope.cns.fr, web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 3529.f For
more information about this cluster, see
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cgi-bin/cluster.cgi?seq=CSOACO23DAO5QP1&cluster=3529.f. Contac
Feng Liang Email: filangelifetech.com URL:
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope
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Lii, W.B., Gruber, C., Jessee, J. and Polayes, D. Unpull-length cDNA libraries and normalization Unpublished (2001)
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24.3%; Score 700.2; DB 13;
Best Local Similarity 94.0%; Pred. No. 1.9e-107;
Matches 755; Conservative 22; Mismatches 20;
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2471 GGAGAGTGAAGCGGGGGTCCCAGCCCTGGTGGGCCCC
                         GGAGAGTGAAGCGGGGGTCCCAGNCCCTGGTGGCCC
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/db_xref="taxon:9606"
/clone="CS0DC023YB10"
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       Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0BAF004ZD01_AF00293_1.
Location/Qualifiers
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/note="1st strand cDNA was primed with a Not1-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
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Invitrogen. This sequence belongs to sequence cluster 3529.f For more information about this cluster, see
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi/seq=C80AC023DA05QP2&cluster=3529.f. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSOAC023DA05QP2.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-970-944-2 Perfect score: Title:

1 MAVRPGLWPALLGIVLAAWL.......AVAGLGQPDAGLFTVSEAEC 899 Sequence:

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1586107 seqs, 282547505 residues Searched:

1586107 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp2003as:\* geneseqp2003bs:\* geneseqp1980s:\* geneseqp1990s:\* geneseqp2000s:\* geneseqp2001s:\* geneseqp2002s:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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## SUMMARIES

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## ALIGNMENTS

Human; NOVX polypeptide; cardiomyopathy; atherosclerosis; cancer; cell signal processing; metabolic pathway modulation; cancerous tissue; antibody; diabetes; transgenic animal; UNCS-like protein; NOV1; chromosome 13. AAU79939 standard; protein; 899 AA. Human UNC5-like protein NOV1. (first entry) 15-JUL-2002 AAU79939; RESULT 1 AAU79939 

Homo sapiens.

WO200229038-A2.

11-APR-2002.

04-OCT-2001; 2001WO-US031377.

04-OCT-2000; 2000US-0237862P.

(CURA-) CURAGEN CORP.

Shimkets RA; Herrmann JL, Rastelli L,

WPI; 2002-340104/37. N-PSDB; ABK49422.

Novel isolated NOVX polypeptide, and encoded polynucleotide, useful for treating cardiomyopathy, artherosclerosis, and cancer.

Claim 1; Page 9; 180pp; English.

The present invention relates to a new NOVX polypeptide having a 900 (NOV1), 4349 (NOV2), 940 (NOV3), 798 (NOV4), 865 (NOV5), or 331 (NOV6) residue amino acid sequence, as given in the specification. The novel polypeptide, and its encoding polymucleotide, are used to treat cardiomyopathy, atherosclerosis, cancer or a disease related to cill signal processing and metabolic pathway modulation, in a human. Detecting the polypeptide or polymucleotide is useful for identifying cancerous tissue. The antibody can be used to treat diabetes or cancer. The host screening. The present amino acid sequence is that of the human UNC5-like protein NOV1 of the invention. This sequence is encoded by the human UNC5

(first entry)

21-MAY-2002

AAU85403;

Human protein NOV1

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WKSKLLVSYQEIPFYHIWNGTQRYLHCTFTLERVSPSTSDLACKLWVWQVEGDGQSFSIN 780
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AAU85403 standard; protein; 898 AA

RESULT 2
AAU85403
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The invention relates to an isolated cytoplasmic, nuclear, membrane common, or secreted polypeptide (NOVX, x= 1-14) their variants or mature bound, or secreted polypeptide (NOVX, x= 1-14) their variants or mature comprising the nucleic acid, a cell comprising the vector, an anti-convector comprising the nucleic acid and the NOVX antibody and modulators of NOVX. NOVX, the nucleic acid and the antibody are useful for treating or preventing a NOVX-associated antibody are useful for treating or preventing a NOVX-associated disorder, where the disorder is selected from cardiomyopathy.

CC disorder, where the disorder is selected from cardiomyopathy, can metabolic pathway modulation, metabolic disorders, obssity, concertassociated cachexia, cancer, infectious disease, anorexia, cancer-associated cachexia, cancer, confimume disorders, haematopoletic disorders, and the various immune disorders metabolic disorders associated with obesity, the dyslipidaemias, metabolic disorders associated with obesity, the chisasses, bacterial, fungal, protecal and viral infections, pain, bullmia, asthma, hypertension, urinary retention, osteoporosis, Cdiseases, multiple sclerosis, Albright Hereditary Osteoporosis, Conservation, urinary retention, osteoporosis, Conservation, uninary retention, osteo
                                                                                                                                  Human, NOVX, cardiomyopathy; atherosclerosis; diabetes; obesity; infection; cell signal processing disorder; metabolic disorder; obesity; infection; ancer.associated cachexia; cancer. neurodegenerative disorder; Alzheimer.s disease; Parkinson's disease; immune disorder; haematopoietic disorders; dyslipidaemia; pain; asthma; hypertension; osteoporosis; Crohn's disease; multiple sclerosis; angina pectoris; myocardial infarction; uller; allergy; benign prostatic hypertrophy; psychosis; neurological disorder; anxiety; schizophrenia; manic depression; dementia; dyskinesia; Huntington's disease; Gilles de la Tourette's syndrome; gene therapy.
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Smithson (
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04-AUG-2000; 2000US-0223752P.
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04-AUG-2000; 2000US-022370P.
14-AUG-2000; 2000US-0225140F.
15-AUG-2000; 2000US-0225392P.
15-AUG-2000; 2000US-0225392P.
16-AUG-2000; 2000US-0225470P.
16-AUG-2000; 2000US-0225697P.
01-FEB-2000; 2000US-022662P.
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such as Huntington's disease and Gilles de la Tourette's syndrome. The nucleic acid is useful in gene therapy. The present sequence represents
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Netrin binding membrane receptor; receptor; UNC5H-1; human; nootropic; neuroprotective; cytostatic; antiparkinsonian; cerebroprotective; cancer; central nervous system; CNS; stroke; Parkinson's disease; multiple sclerosis; Alzheimer's disease.
                                       Human netrin binding membrane receptor UNC5H-1 protein.
                                                                                                                                          domain"
                                                                                                                            "Thrombospondine type 1 domain
                                                                                                              'note= "Immunoglobulin domain
                                                                                                                                                      "Transmembrane region"
                                                                                                                                                                               'note= "Death domain"
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                                                                                                  Location/Qualifiers
                                                                                                                                                                   'note= "ZUS domain"
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                                                                                                                                                                                                                    15-OCT-2001; 2001WO-EP011891.
AAU97899 standard; protein;
                          (first entry)
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718

This invention relates to the DNA and protein sequences of a novel

purified human netrin binding membrane receptor, UNC5H-1. The DNA

sequence of the invention is useful as a probe for detecting a nucleic

acid encoding the UNC5H-1 protein in a biological sample. The sequences

of the invention are useful to screen for agents which decrease the

cof the invention are useful to screen for agents which decrease the

correction agents which regulate (modulate) the activity of the protein of

the invention. A pharmaceutical composition containing the protein of

the invention or a reagent that modulates the activity of the UNC5H-1 protein

compared to a central nervous system (CNS) disorders (e.g., Parkinson's

disease, multiple salerosis, stroke and Alzheimer's disease). Fusion

proteins comprising the UNC5H-1 protein are useful for generating

antibodies and for in various assay systems, and the protein can be used

contained the invention is useful for detecting a coding sequence for the UNC5H
contained the invention is useful for detecting a coding sequence for the UNC5H
contained the invention binding

contained the invention of the invention

Novel human netrin binding membrane receptor polypeptide and polynucleotides for identifying modulating agents useful in treating diseases e.g. Parkinson's disease, multiple sclerosis, stroke, Alzheimer's disease.

Claim 1; Fig 2; 94pp; English.

Sequence 898 AA;

RESULT 3 AAU97899

Query Match

Length 898; DB 5; Score 4688.5; 97.98;

UNC-5 homologue UNC5H-1

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                                                                                     VLLVCKAVPATQIFFKCNGEWVRQVDHVIERSTDGSSGEPTMEVRINVSRQQVEKVFGLE
                                                                                                     61 VLLVCKAVPATQIPFKCNGEWVRQVDHVIERSTDGSSGLPTMEVRINVSRQQVEKVFGLE
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                                  1 MAVRPGLWPALLGIVLAAWIRGSGAQQSATVANPVPGANPDLLPHFLVEPEDVYIVKNKP
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AAW78898 standard; protein; 898

(revised)
(first entry)

25-MAR-2003 21-DEC-1998

AAW78898;

AAW78898 ID AAW7 XX AC AAW7 XX DT 25-W DT 21-C

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UNC5H-1 and UNC5H-2 (see AAW78900) are rat homologues of Caenorhabditis clegans UNC-5 protein. Their amino acid sequences were deduced from clear isolated unc5h cDNA clones (see AAV52940 and AAV52945) isolated from an isolated uncbh cDNA library. The predicted proteins show similarity with UNC-CC isobsses 2 predicted ig-like domains and 2 predicted thrombospondin type-1 repeats, a predicted membrane spanning region, and a large contractellular domain. They are predicted to be involved in cell migration and axon guidance, and are characterised as receptor proteins for netrins. Human UNC5H-1 (see AAW78899) and UNC5H-2 (see AAW78901) proteins contransfected host cells. The invention also provides unc-5 from transfected host cells. The invention also provides unc-5 hybridisation probes and primers, vertebrate UNC-5-specific binding compositions in diagnosis (e.g. genetic hybridisation screens for vertebrate unc-5 gene expression) and in the biopharmaccutical industry composition expression and in the biopharmaccutical industry correcting chemical libraries for modulating cell guidance, reagents for modulating cell guidance, reagents for gene (e.g. agents, etc.).

C (Updated on 25-MAR-2003 to correct PI field.)
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/note= "peptide used to raise rabbit polyclonal antisera"
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                      UNC-5; UNC5H-1; rat; netrin receptor; cell migration; axon guidance;
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94.7%; Pred. No. 0;
ive 19; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                        Netrin-binding, vertebrate proteins
                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 19-22; 32pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                         the biopharmaceutical industry
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N-PSDB; AAV52940.
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                                            diagnosis; therapy
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              VNGGWSTWTEWSVCSASCGRGWQKRSRSCTNPAPLNGGAPCBGQNV-QKTACATLCPVDG 299
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                                    SWSPWSKWSACGLDCTHWRSRECSDPAPRNGGEECQGTDLDTRNCTSDLCVHSASGPEDV
                                                                        ALYVGLIAVAVCLVLLLLVLILVYCRKKEGLDSDVADSSILTSGFQPVSIKPSKADNPHL
                                                                                 LIIQPDLS-TITIYQGSLCPRQDGPSPKFQLINGHLLSPLGGGRHTLHHSSPISEAEEFV
                                                                                                                             LTIQPDLSTTTTYQGSLCSRQDGPSPKFQLSNGHLLSPLGSGRHTLHHSSPTSEADFV
                                                                                                                                               SRLSTQNYFRSLPRGTSNMTYGTFNFLGGRLMIPNTGISLLIPPDAIPRGKIYEIYLTLH
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AAU10543 standard; protein; 898
           (first entry)
           14-FEB-2002
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YSG; YSG7; schizophrenia, chronic animal model; LCGU; netrin receptor; local cerebral glucose utilisation; phosphodiesterase 1-alpha; UNCSH1; calcium-independent alpha-latrotoxin receptor; CIRL; trkE; synapsin 1A; epithelial discoidin domain receptor 1; synapsin 1B; neuroleptic; Rat netrin receptor UNC5H1 (YSG7) polypeptide. tūmour necrosis factor alpha; TNF-alpha; rat

WO200175440-A2. Rattus

11-OCT-2001

02-APR-2001; 2001WO-GB001486

31-MAR-2000; 2000GB-0007880. 26-MAY-2000; 2000GB-00012768.

(WELF-) WELFIDE CORP.

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diagnoshing and/or developing treatments for schizophrenia using chronic animal models. The polymucleotides and their encoded polypeptides are used for identification of compounds which modulate the expression of YSG molecules, leading to the manufacture of schizophrenia medicaments. The sequences can also be used for testing candidate compounds for any effect on the polypeptides. Anti-schizophrenic effects of a compound can be determined by measuring local cerebral glucose utilisation (LCGU) or comparing its expression level with that of a control group. The comparing its expression level with that of a control group. The sequences are useful in the identification of genes associated with collipse and in the development of an antibody. The sequences of the invention include phosphodiesterase 1-alpha, calcium-independent caepptors (CIRL)-1,2&3, epithelial discoidin domain receptor (CIRL)-1,2&3, epithelial discoidin domain treceptor (TRE), netrin receptor (UNCSHI), synapsins lA and AB and terrin receptor (TRF) alpha. This sequence represents rat netrin
                                                                                                                                               for identifying anti-
                                                                                                                                      Novel chronic animal model of schizophrenia, useful for identify; psychotic drugs and genes that are associated with schizophrenia.
                                                                                                                                                                                                                                                         invention relates to YSG polynucleotide fragments for
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                               Pratt
                               Morris B,
                       Ohashi Y,
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                                                                       WPI; 2002-010813/01
                                                                                                                                                                                                    Disclosure; Fig 8b;
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                       Cochran S,
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Sequence 898 AA;

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3, 180 120 420 240 9 9 479 VLL VCKAVPATQI FFKCNGEWVRQVDHVI BRSTDGSSGEPTMBVRINVSRQQVEKVFGLE EYWCQCVAWSSSGTTKSQKAYIRIARLRKNFEQEPLAKEVSLEQGIVLPCRPPEGIPPAE 1 MAVRPGLWPALLGIVLAAWIRGSGAQQSATVANPVPGANPDLLPHFLVEPEDVYIVKNKP 121 BYWCQCVAWSSSGTIKSQKAYIRIAYLRKNFBQEPLAKEVSLEQGIVLPCRPPEGIPPAE 181 VEWLRNEDLVDPSLDPNVYITREHSLVVRQARLADTANYTCVAKNIVARRRSTSAAVIVY VEWLRNEDLVDPSLDPNVYITREHSLVVRQARLADTANYTCVAKNIVARRRSASAAVIVY VNGGWSTWTEWSVCSASCGRGWQKRSRSCTNPAPLNGGAFCEGQNVHDRTVSSLLVSVDG SWSPWSKWSACGLDCTHWRSRECSDPAPRNGGEECQGTDLDTRNCTSDLCVHSASGPEDV Gaps ALYVGLIAVAVCLVLLLLVLILVYCRKKEGLDSDVADSSILTSGROPVSIKRSKADNPHL LTIQPDLS-TTTTYQGSLCPRQDGPSPKFQLTNGHLLSPLGGGRHTLHHSSPTSEABEFV LTIOPDLSTTTTTYGGSLCSRODGPSPKFQLSNGHLLSPLGSGRHTLHHSSPTSEAEDFV SRLSTQNYFRSLPRGTSNMTYGTFNFLGGRLMIPNTGISLLIPPDAIPRGKIYEIYLTLH KPEDVRLPLAGCQTLLSPIVSCGPPGVLLTRPVILAMDHCGEPSPDSWSLRLKKQSCEGS SRLSTQNYFRSLPRGTSNWAYGTFNFLGGRLMIPNTGISLLIPPDAIPRGKIYEIYLTH . 9 Length 898; Indels 26; DB 5; 95.0%; Score 4545.5; 94.7%; Pred. No. 0; iive 19; Mismatches Matches 852; Conservative Local Similarity Н 61 181 Query Match 121 300 360 120 480 480 540 301 361 121

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à D  $\stackrel{>}{\circ}$ 셤 à QQ ò g à a  $\delta$ 

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Netrin binding membrane receptor; receptor; UNC5H-1; Rat; nootropic; neuroprotective; cytostatic; antiparkinsonian; cerebroprotective; cancer; central nervous system; CNS; stroke; Parkinson's disease; multiple sclerosis; Alzheimer's disease.
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                                                                                                                          NFNITKDTRFAELLALESEAGVPALVGPSAFKIPFLIRQKIISSLDPPCRRGADWRTLAQ
                                                                                                                                             NFNITKDTRFAELLALESEGGVPALVGPSAFKIPFLIRQKIIASLDPPCSRGADWRTLAQ
                                                                                                                                                                   KLHLDSHLSFFASKPSPTAMILNLWEARHFPNGNLSQLAAAVAGLGQPDAGLFTVSEAEC
                                                                                                                                                                               KLHLDSHLSFFASKPSPTAMILNLWEARHFPNGNLGQLAAAVAGLGQPDAGLFTVSEAEC
WEQDVIHLGEEAPSHLYYCQLEASACYVFTEQLGRFALVGEALSVAAAKRLKLLLLFAPVA
           LWKSKLLVSYQEIPFYHIWNGTQRYLHCTFTLERVSPSTSDLACKLWVWQVEGDGQSFSI
                                                                                              treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel human netrin binding membrane receptor polypeptide and polypucleotides for identifying modulating agents useful in tr diseases e.g. Parkinson's disease, multiple sclerosis, stroke,
                                          CTSLEYNIRVYCLHDTHDALKEVVQLEKQLGGQLIQEPRVLHFKDSYHNLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                         302. .348
/note= "Thrombospondine type 1 domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                "Thrombospondine type 1 domain
                                                                                                                                                                                                                                                                                                           Rat netrin binding membrane receptor UNCSH-1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                          "Immunoglobulin domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Transmembrane region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Death domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     495. .598
/note= "ZU5 domain"
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                                                                                                                                                                                                                                              AAU97900 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                  152. .223
/note= "Im
247. .294
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This invention relates to the DNA and protein sequences of a novel

cutified human netrin binding membrane receptor, UNCSH-1. The DNA

cutified human netrin binding membrane receptor, UNCSH-1. The DNA

sequence of the invention is useful as a probe for detecting a nucleic

acid encoding the UNCSH-1 protein in a biological sample. The sequences

of the invention are useful to screen for agents which decrease the

cutivity of the UNCSH-1 protein. The sequences are also useful for

screening agents which regulate (modulate) the activity of the protein of

the invention. A pharmaceutical composition containing the protein of the

cutivity of the UNCSH-1 protein

can be useful for treating a UNCSH-1 dysfunction related disease such as

cancer or a central nervous system (CNS) disorders (e.g., Parkinson's

cancer or a central nervous system (CNS) disorders (e.g., Parkinson's

disease, multiple sclerosis, stroke and Alzheimer's disease). Fusion

cropic antibodies and for in various assay systems, and the protein can be used

as a bait protein in a two-hybrid assay or three-hybrid assay. The method

cof the invention is useful for detecting a coding sequence for the UNCSH-1

cof the invention is useful for detecting a coding sequence for the UNCSH-1

cof the invention of the invention of the invention 61 VLLVCKAVPATQIFFKCNGEWVRQVDHVIERSTDSSSGLPIMEVRINVSRQQVEKVFGLE EYWCOCVAWSSSGTTKSOKAYIRIARLRKNFEQEPLAKEVSLEQGIVLPCRPPEGIPPAE 61 VLLVCKAVPATQIFFKCNGEWVRQVDHVIERSTDGSSGEPTMEVRINVSRQQVEKVFGLE 1 MAVRPGLWPALLGIVLAAWLRGSGAQOSATVANPVPGANPDLLPHFLVEPEDVYIVKNKP 1 MAVRPGLMPVLLGIVLAAMLRGSGAQQSATVANPVPGANPDLLPHFLVEPEDVYIVKNKP Gaps 3; Length 898; Indels DB 5; 26; 95.0%; Score 4545.5; 94.7%; Pred. No. 0; ive 19; Mismatches Matches 852; Conservative Local Similarity Sequence 898 AA; 121 Query Match 

420 ALYIGLVAVAVCEFLILLALGLIYCRKKEGLDSDVADSSILTSGFQPVSIKPSKADNPHL 419 LTIQPDLS-TTTTYQGSLCPRQDGPSPKFQLTNGHLLSPLGGGRHTLHHSSPTSEAEBFV 479 599 120 180 09 SRLSTQNYFRSLPRGTSNMTYGTFNFLGGRLMIPNTGISLLIPPDAIPRGKIYBIYLTLH 540 KPEDVRLPLAGCQTLLSPVVSCGPPGVLLTRPVILAMDHCGEPSPDSWSLRLKKQSCEGS VNGGWSTWTEWSVCSASCGRGWQKRSRSCTNPAPLNGGAFCEGQNVHDRTVSSLLVSVDG SWSPWSKWSACGLDCTHWRSRECSDPAPRNGGEECQGTDLDTRNCTSDLCVHSASGPEDV ALYVGLIAVAVCLVLLLLVLILVYCRKKEGLDSDVADSSILTSGFQPVSIKPSKADNPHL LIIQPDLSTITITYQGSLCSRQDGPSPKFQLSNGHLLSPLGSGRHTLHHSSPTSEAEDFV SKLSTQNYFRSLPRGTSNWAYGTFNFLGGRLMIPNTGISLLIPPDAIPRGKIYEIYLTLH KPEDVRLPLAGCQTLLSPIVSCGPPGVLLTRPVILAMDHCGEPSPDSWSLRLKKQSCEGS VEWLRNEDLVDPSLDPNVYITREHSLVVRQARLADTANYTCVAKNIVARRRSASAAVIVY 121 241 301 300 361 360 421 420 480 480 540 181 241 g ð 음 ∂ g ò g 원 à g ò qq dd ð ò à d ò ò

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WEQDVLHLGEEAPSHLYYCQLEASACYVFTEQLGRFALVGEALSVAAAKRLKLLLFAPVA

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Disclosure; Fig 3; 94pp; English

CTSLEYNIRVYCLHDTHDALKEVVQLEKQLGGQLIQEPRVLHFKDSYHNLRLSIHDVPSS

599 629

LWKSKLLVSYQEIPFYHIWNGTQRYLHCTFTLERVSPSTSDLACKLWVWQVEGDGQSFSI

720 719 780

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KLHLDSHLSFFASKPSPTAMILNLWEARHFPNGNLSQLAAAVAGLGQPDAGLFTVSEAEC

840 179

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839

NFNITKDTRFAELLALESEAGVPALVGPSAFKIPFLIRQKIISSLDPPCRRGADWRTLAQ

839 838 899 898

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WPI; 2001-476283/
N-PSDB; AAK52261
                                                    WO200157190-A2
                                                                       27-APR-2000;
20-JUN-2000;
19-JUL-2000;
01-SEP-2000;
                                                                                 15-SEP-2000;
                                                                                      30-NOV-2000;
                                                                    03-FEB-2000;
                        06-NOV-2001
                                                                                                   Zhao
                                                          09-AUG-2001
                                                                                                Tang YT,
Ma Y, Zhi
Xue AJ,
                   AAM79128;
                                               Homo
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Human; cytokine; cell proliferation; cell differentiation; gene the vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation.
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ao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang
Yang Y, Wejhrman T, Goodrich R;
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; 2000US-00560875.
; 2000US-00590075.
; 2000US-00624936.
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; 2000US-00654936.
; 2000US-00654936.
                                                                                                                                                     Human protein SEQ ID NO 1790.
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AAM79128 standard; protein;
                                                                                                      (first entry)
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Yang Y,
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therapy;

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The invention relates to polymucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell prollferation or cell forbulations. The production of other cytokines in other cell populations. The polymucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, activity, tissue growth factor activity, immunoomodulatory activity and activity, immunoomodulatory activity and activity in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication
                                                                                                                                                                                                                                                                    Nucleic acids encoding polypeptides with cytokine-like activities, useful
Zw.;
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                                                                                                                                                 77 VLLVCKAVPATQIPFKCNGEWVRQVDHVIERSTDGSSGLPTMEVRINVSRQQVEKVFGLE
                                                                                                                                                                                          1 MAVRPGLWPALLGIVLAAWLRGSGAQQSATVANPVPGANPDLLPHFLVEPEDVYIVKNKP
                                                                                                      MTRRPSL-----MAGROHGWSAQQSATVANPVPGANPDLLPHFLVEPEDVYIVKNKP
                                                                                                                                                                          EYWCQCVAWSSSGTTKSQKAYIRIARLRKNFEQEPLAKEVSLEQGIVLPCRPPEGIPPAE
                                                                                                                                                                                                                         VEWLRNEDLVDPSLDPNVYITREHSLVVRQARLADTANYTCVAKNIVARRSASAAVIVY
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                                      Length 943;
                                                            Indels
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                                     DB 4;
                                                           4; Mismatches
                                   Score 4434;
Pred. No. 0;
                                  Query Match 92.6%;
Best Local Similarity 90.4%;
Matches 853; Conservative
           Sequence 943 AA;
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Sequence 842

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AAU74818 standard; protein; 842 AA
                                                                                                            21-JUN-2000; 2000US-0214027P.
25-AUG-2000; 2000US-0228045P.
12-DEC-2000; 2000US-0255104P.
                                                                                                      21-JUN-2001; 2001WO-US019942
                                                                                                                           (INCY-) INCYTE GENOMICS INC.
                 (first entry)
                         REPTR 1 protein.
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                                                                                                                                                    WPI; 2002-090432/12
                                                                                                                                                        N-PSDB; ABK15169
                                                                                        WO200198354-A2
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                                                                                 sapiens.
                  23-APR-2002
          AAU74818;
                                                                                 Homo
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Matches 838;
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                                                                                                                                                                                      AREPTR; human; antiinflammatory; cytostatic; immunosuppressive; antiviral; antial-HIV; antiarthritic; anticonvulsant; nootropic; neuroprotective; antiallergic; antibody; immunogen; endometriosis; gastrointestinal disorder; gastriitis; oesophageal carcinoma; crohn's disease; irritable bowel syndrome; ulcerative colitis; endocrine disorder; hypothalamus disorder; Kallman's disease; autoimmune disease; inflammatory disease; infertility; receptor; acquired immune deficiency syndrome; AIDS; rheumatoid arthritis; allergy; osteoarthritis; diabetes mellitus; multiple sclerosis; systemic lupus erythematosus; cell proliferative disorder; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tang YT;
Burford N;
Xu Y;
Lu Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Twelve human receptors (referred to as REPTR-1 to REPTR-12), useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the diagnosis, treatment and prevention of gastrointestinal (e.g. gastritis), autoimmune/inflammatory (e.g. osteoarthritis) and cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                       developmental disorder; Duchenne muscular dystrophy;
Becker muscular dystrophy; neurological disorder; epilepsy;
Alzheimer's disease; Huntington's disease; reproductive disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nguyen DB,
R, Yao MG,
I C, Yang J,
Duggan BM,
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                                                                                                             61 VLLVCKAVPATQIFFKCNGEWVRQVDHVIERSTDGSSGLPTMEVRINVSRQQVEKVFGLE
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Score 4379.5;
Pred. No. 0;
                                          1; Mismatches
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  91.5%;
93.1%;
                                                 Conservative
                        Similarity
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462 120 522 180 582 240 642 299 702

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(first entry)

(revised)

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Netrin-binding, vertebrate proteins - useful for diagnosis, the biopharmaceutical industry.
                                                                                                                                                                                                                                             Claim 1; Page 22-23; 32pp; English.
                Human UNC-5 homologue UNC5H-1
                                                                                                                                                                                          (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                                                                                                                                                           (e.g. as immunogens,
screening chemical li
                                diagnosis; therapy.
                                                                                                                                                                                                               1998-495364/42.
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                                                                   Misc-difference
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                                                                                                                                 Misc-difference
                                                                                                                                                                                                                                                                                                                                                                 Sequence 556 AA;
                                          Homo sapiens
                                                                                                                                                                                19-FEB-1997;
                                                                                                                                                 WO9837085-A1
                                                                                                                                                                      19-FEB-1998;
 25-MAR-2003
21-DEC-1998
                                                                                                                                                           27-AUG-1998
                          UNC-5;
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98WO-US003143, 97US-00808982

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Three variants of human unc-5C cDNAs (unc-5Cb, unc-5Cc and unc-5C8) and a human unc-5HS1 cDNA, useful in yeast two hybrid experiments for
                                                                                                                                       61 GRQPVSIKPSKADNPHLLITIOPDLSTTTTTYGGSLCPRQDGPSPKFQLTNGHLLSPLGGG
                                                                                                                                                                                                                                                NCTSDLCVHSASGPEDVALYVGLIAVAVCLVLLLVLILVYCRKKEGLDSDVADSSILTS
                           1 NCTSDLXVHTASGPEDVALYVGLIAVAVCLVLLILVLILVYCRKKEGLDSDVADSSILTS
                                                                                                      GFQPVSIKPSKADNPHLLTIQPDLS-TTTTYQGSLCPRQDGPSPKFQLTNGHLLSPLGGG
                                                                                                                                                                                                            RHTLHHSSPTSEAEEFVSRLSTQNYFRSLPRGTSNMTYGTFNFLGGRLMI PNTGI SLLIP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human, Caenorhabditis elegans, UNC-5; splice variant; nematode worm; protein-protein interaction; identification.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB50691 standard; protein; 931 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            UNC5H-1 and UNC5H-2 (see AAW78901) are human homologues of Caenorhabditis elegans UNC-5 protein. Their amino acid sequences were deduced from solutions to the cones (see AAV52941 and AAV52943) isolated from an embryonic brain cDNA library. The predicted proteins show similarity with UNC-5, possess 2 predicted membrane spanning region, and a large intracellular domain. They are predicted to be involved in cell migration and axon guidance, and are predicted to be involved in cell migration certains. Rat UNC5H-1 (see AAW78998) and UNC5H-2 (see AAW78900) proteins centains. Rat UNC5H-1 (see AAW78998) and UNC5H-2 (see AAW78900) proteins are also claimed. Vertebrate UNC-5 proteins may be produced recombinantly comparisation probes and primers, vertebrate UNC-5-specific binding subject compositions in diagnosis, (e.g. genetic hybridisation screens for vertebrate unc-5 gene expression) and in the biopharmaceutical industry compositions conserved the compositions of the composition and in the biopharmaceutical industry compositions conserved the compositions of the composition and in the biopharmaceutical industry compositions conserved the compositions of the composition and in the biopharmaceutical industry compositions conserved the compositions cons
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                                                                                UNC5H-1; human; netrin receptor; cell migration; axon guidance;
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S8.3%; Score 2789; DB 2; Length 556;
Best Local Similarity 96.6%; Pred. No. 4.5e-233;
Matches 538; Conservative 1; Mismatches 16; Indels ;
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Masu M,

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Hinck

Leonardo ED,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CVAWSSSGTTKSQKAYIRIARLRKNFEQEPLAKEVSLEQGIVLPCRPPEGIPPAEVEWLR 185
                                                                           The present invention describes 3 variants of human unc-5C cDNAs (unc-5Cb, unc-5Cc and unc-5C8) which correspond to alternatively spliced unc-5Cb, ranscripts, and a human unc-1813 cDNA which shares howology with the Rattus norvegicus unc-5H31 cDNA. Also described are assays based on protein-protein-interactions between the unc-5 protein and a variety of different interacting proteins. The unc-5C variant cDNAs and unc-5H31 cDNA are useful in methods for identifying compounds which reduce or inhibit the lethal phenotype associated with the expression of the unc-5 death domain in yeast. They are also useful in yeast two hybrid death domain in yeast. They are also useful in yeast two hybrid that interact with the human unc-5C protein. AAC90914 to AAC90971 and AAB50646 to AAB50693 represent sequences used in the exemplification of
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unknown human cDNAs which encode proteins that interact with
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STWIEWSVCNSRCGRGYQKRIRICINPAPLNGGAFCEGOSV-QKIACTTLCPVDGRWIPW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SKWSACGLDCTHWRSRECSDPAPRNGGEECQGTDLDTRNCTSDLCVHSASGPEDVALYVG
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                                                                                                                                                                                                                                                                                                                                                                                                            9 PALLGIVLAAWLRGSGAQQS---ATVANPVPGANPDLLPHFLVEPEDVYIVKNKPVLLVC
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                                                                                                                                                                                                                                                                                                                                               DB 4; Length 931;
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                                                     Disclosure; Page 224-227; 246pp; English.
                      human unc-5C protein.
                                                                                                                                                                                                                                                                                   the present invention
                                                                                                                                                                                                                                                                                                                     Sequence 931 AA;
        identifying
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The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially compound that regulates the activity of one or more of the compound that regulates the activity of one or more of the composition, a method for identifying a compound composition, a cuttivity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating
                                                              825
                                                                                            857
                                                                                                                            882
                                                                                                                                              New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
                                                              766 WVWQVEGDGQSFSINFNITKDTRFAELLALESEAGVPALVGPSAFKIPFLIRQKIISSLD
                                                                                  826 PPCRRGADWRTLAQKLHLDSHLSFFASKPSPTAMILNLWEARHFPNGNLSQLAAAVAGLG
YHNLRLSIHDVPSSLWKSKLLVSYQEIPFYHIWNGTQRYLHCTFTLERVSPSTSDLACKL
                Human; pain; neuronal tissue; gene therapy;
spinal segmental nerve injury; chronic constriction injury; CCI;
spared nerve injury; SNI; Chung.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Costigan M;
                                                                                                                                                                                                                                                                                                                                                                                                         Human Protein AAC67491, SEQ ID NO 9033.
                                                                                                                                                                                                                                                                                                              ADE63098 standard; protein; 931 AA
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01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-033347P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-AUG-2002; 2002WO-US025765
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                                                                                                                                                                                               QPDAGLFTVSEAE 898
                                                                                                                                                                                                                               RHETWVSLAAEGQ 930
                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENBANK; AAC67491.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO2003016475-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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compound that
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pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polymucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (CMI), chronic constriction injury (CMI) and spared nerve injury (SMI) in an animal (e.g. gene therapy). The sequence presented is a human protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: Specification, but was obtained in electronic form directly from WIPO at
                                                                                                                                                                                                                                                                                       125
                                                                                                                                                                                                                                                                                                                                    CVAWSSSGTIKSQKAYIRIARLRKNFEQEPLAKEVSLEQGIVLPCRPPEGIPPAEVEWLR 185
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                                                                                                                                                                          Query Match 55.8%; Score 2673.5; DB 7. Best Local Similarity 55.5%; Pred. No. 1.1e-222; Matches 507; Conservative 154; Mismatches 221;
                                                                                                                    ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                 Sequence 931 AA;
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed correct corr
                       APQTRGHDWRMLAHKLNLDRYLNYFATKSSPTGVILDLWEAQNFPDGNLSMLAAAVLEEMG 917
PPCRRGADWRTLAQKLHLDSHLSFFASKPSPTAMILNLWEARHFPNGNLSQLAAAVAGLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                    1) chromosome mapping; gene mapping; gene therapy, forensic; supplement; medical imaging; diagnostic; genetic disorder.
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Pred. No. 1.3e-222;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          electronic format directly from WIPO at
ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                   Novel human diagnostic protein #11542.
                                                                                                                                                                                                                                                      A.
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2000US-00649167.
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Best Local Similarity
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23-AUG-2000;
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Rat Protein AAB57679, SEQ ID NO 9031.
29-JAN-2004 (first entry)
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                           KAVPATQIFFKCNGEWVRQVDHVIERSTDGSSGEPTMEVRINVSRQQVEKVFGLEBYWCQ
                                                            CVAWSSSGTTKSQKAXIRIARLRKNFEQEPLAKEVSLEQGIVLPCRPPEGIPPAEVEWLR
                                                                                            STWIEWSVCSASCGRGWOKRSRSCTNPAPLNGGAFCEGONVHDRTVSSLLVSVDGSWSPW
                                                                                                                                                            YHNLRLSIHDVPSSLWKSKLLVSYQEIPFYHIWNGTQRYLHCTFTLERVSPSTSDLACKL
                 PALLGIVLAAWLRGSGAQQS---ATVANPVPGANPDLLPHFLVEPEDVYIVKNKPVLLVC
                                                                                                                  NEDLVDPSLDPNVYITREHSLVVRQARLADTANYTCVAKNIVARRRSASAAVIVYVNGGW
                                                                                                                                                                                 SKWSACGLDCTHWRSRECSDPAPRNGGEECQGTDLDTRNCTSDLCVHSASGPEDVALYVG
  31;
   221; Indels
   Mismatches
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ADE63096 standard; protein; 945 AA.

ADE63096

RESULT 13
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ID ADE63
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The invention discloses a composition comprising two or more isolated rat or human polynuclectides or a polynuclectide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynuclectide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a comprising the vector of the identifying a nucleotide sequence that increases or decreases the expression of the polynucleotide sequence that increases or decreases the expression of the polynucleotide sequence which is differentially expressed in neuronal tissue of a first animal composition of the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the composition, a method for producing a pharmaceutical composition, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more continued that the sequence presented for identifying a compound useful in treating conductates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (SNI)) in an animal (e.g. gene therapy). The sequence presented is a rat protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: the sequence data for this patent did not form directly from WIPO at the print of the pri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        two or more isolated polypeptides, useful for treating pain in an animal.
in; neuronal tissue; gene therapy; spinal segmental nerve injury; constriction injury; CCI; spared nerve injury; SNI; Chung.
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Best Local Similarity 52.0%; Pred. No. 2007 236;
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01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
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GENBANK; AAB57679.
                                                                                                                                     Rattus norvegicus
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                pain;
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                                                                                                                                          TVCPVDGAWTEWSKWSACSTECAHWRSRECMAPPPQNGGRDCSGTLLDSKNCTDGLCVLN 356
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                                       EGI PPAEVEWLRNEDLVDPSLDPNVYITREHSLVVRQARLADTANYTCVAKNIVARRRSA
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The invention describes an isolated polypeptide (I), useful in the manufacture of a medicament for treating a syndrome associated with a human disease. (I), the polynucleotide encoding it (II) and an antibody (III) to (I) are useful for treating or preventing cancer, metabolic disorders, skin disorders, infectious disease, anorexia, behavioral disorders, anxiety disorders, bendocrine disorders, heart and blood disorders, anxiety disorders, practices, inflammatory disorders, neurodegenerative disorder, Alzheimer's disease, Parkinson's disorder, immune disorders, heamatopoletic disorders, and the various dyslipidaemias, metabolic disturbances associated with obsorie, and the metabolic syndrome X and wasting disorders associated with chronic diseases. (I), (II) or (III) are useful in screening assays, detection assays (e.g., chromosomal mapping, tissue typing, forensic biology), predictive medicine (e.g., diagnostic assays and prognostic assays), in methods of treatment (e.g., therapeutic and prophylactic). (I) is creen for not not and in the antibodies immunospecific for (I), to creen for not not and in the antibodies immunospecific for (I), to
                          disorder;
                 blood disorder; anxiety disorder; brain disorder; inflammatory disorder neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; dyslipidaemia; metabolic disturbance; obesity; metabolic syndrome X; wasting disorder;
         heart disorder;
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Macdougall J;
ES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          screen for potential agonist and antagonist compounds, and as bait protein in a two-hybrid or three-hybrid assay. (II) is useful in gene therapy, to express (I), to detect (I) mRNA or a genetic lesion in a gene, and to modulate activity of (I). A cell containing a vector exressing (I) is useful for producing non-human transgenic animals. The is the amino acid sequence of a novel human polypeptide described in t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel isolated polypeptide, designated NOVX, useful for treating opreventing cancer, diabetes, obesity, dyslipidemia, anorexia, and metabolic, neurodegenerative, immune and hematopoietic disorders.
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       disorder;
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Alsobrook JP, I
V, Ellerman K,
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, Smithson G,
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falyankar UM, Grosse WM,
                                                                                           gene therapy; transgenic animal; human.
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Li L, Edinger S, Ge
Millet I, Stone D,
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2000US-0238125P.
2000US-0238172P.
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Rastelli L,
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blood disor
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Cancer; metabolic disorder; skin disorder; infectious disease; anorexia;

Novel UNCS receptor-like protein.

(first entry)

14-AUG-2002

MXEXEXEXEX EXE

AA.

protein; 946

standard;

ABG61795 ABG61795

RESULT 14

ABG61795

Invention

 $\Xi$ 

UNC-5; UNCSH-2; rat; netrin receptor; cell migration; axon guidance;

Rat UNC-5 homologue UNC5H-2.

diagnosis; therapy

Rattus sp.

(revised)
(first entry)

25-MAR-2003 21-DEC-1998

Location/Qualifiers

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                                                                                              QVEKVFGLEEYWCQCVAWSSSGTTKSQKAYIRIARLRKNFEQEPLAKEVSLEQGIVLPCR
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                                                      1 MGARSGARGALLLALLICWDPRLSQAGRKRSGEVLPDSFPSAPAEPLPYFLQEPQDAYIV
                                                                                KNKPVLLVCKAVPATQ1FFKCNGEWVRQVDHV1ERSTDGSS-----GEPTMEVR1NVSRQ
                                                                                                                                                                             PPEGI PPAEVEWLRNEDLVDPSLDPNVYITREHSLVVRQARLADTANYTCVAKNI VARRR
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          Gaps
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ed. No. 9.7e-207;
Mismatches 247; Indels
Pred. No.
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 52.1%;
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 Similarity
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AAW78900 standard; protein; 943

RESULT 15 AAW78900

AAW78900

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clegans UNC-5 protein. Their amino acid sequences were deduced from isolated unc5h cones (see AAV52940 and AAV52942) isolated from an isolated unc5h cones (see AAV52940 and AAV52942) isolated from an isolated unc5h cones (see AAV52940 and AAV52942) isolated from an isolated unc5h cones (see AAV52940 and AAV52942) isolated from an cone isolated cone is the cone isolated in the cone isolated isolated from the cone isolated isolated in the cone predicted isolated isolated in the cone isolated isolated isolated isolated in the cone isolated 
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52.0%; Score 2490; DB 2;
Best Local Similarity 52.3%; Pred. No. 1.1e-206;
Matches 496; Conservative 144; Mismatches 226;
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                                   SACGLDCTHWRSRECSDPAPRNGGEECQGTDLDTRNCTSDLCV---HSASGPE-----
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Search completed: October 4, 2004, 18:28:53 Job time : 149 secs

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us-09-970-944-2.rai

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October 4, 2004, 18:26:37; Search time 34 Seconds (without alignments) 1365.051 Million cell updates/sec
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(c) 1993 - 2004 Compugen Ltd
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US-08-808-982-7
US-09-306-902A-8
US-09-306-902A-8
US-08-313-28BB-19
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Maximum DB :
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Sequence 2, Appli Sequence 1, Appli Sequence 1, Appli Sequence 13, Appli Sequence 13, Appli Sequence 290, Appli Sequence 290, Appli Sequence 290, Appli Sequence 290, Appli Sequence 294, Sequence 17, 1 Sequence Sequence MEDIUM TYPE: Floppy disk
COMFUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/808,982 US-09-445-027A-1 US-09-930-872-4 US-09-130-491-133 US-09-907-794A-290 US-09-907-794A-290 US-09-907-794A-290 US-09-907-794A-294 US-09-907-794A-294 US-09-907-75A-294 US-09-907-75A-294 US-09-907-75A-294 US-09-902-775A-294 US-09-369-364A-17 ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP STREET: 268 BUSH STREET, SUITE 3200 CLIY: SAN FRANCISCO STATE: CALIFORNIA COUNTRY: USA US-09-963-791-24 US-09-963-791-2 US-08-348-006B-5 -09-568-559-2 -09-130-491-2 95.0%; Score 4545.5; 94.7%; Pred. No. 0; ALIGNMENTS Sequence 5, Application US/08808982
Patent No. 5939271
GENERAL INFORMATION:
APPLICANT: Tessier-Lavigne, Marc
APPLICANT: Heonardo, E. David
APPLICANT: Hink, Lindsay
APPLICANT: Masu, Masayuki
APPLICANT: Kazuko, Keino-Masu
TITLE OF INVENTION: Netrin Receptors
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS: FILING DATE: CAP, 08, 08, 982

CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERNICE/DOCKET NUMBER: UC96-217
TELECOMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS: STRANDEDNESS: not relevant TOPOLOGY: not relevant MOLECULE TYPE: peptide 898 amino acids 837 837 964 967 727 727 608 997 1059 1115 11119 11119 1081 757 757 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy amino acid TYPE: amino a STRANDEDNESS: 94104 160.5 159.5 159.5 159.5 153.5 153.5 153.5 153.5 153.5 153.5 153.5 US-08-808-982-5 LENGTH: US-08-808-982-5 Query Match RESULT 1 

9

Gaps

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26; Indels

19; Mismatches

Best Local Similarity 94.73 Matches 852, Conservative

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Length 898;

1 MAVRPGLWPALLGIVLAAWLRGSGAQOSATVANPVPGANPDLLPHFLVBFBDVYIVKNF

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                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/306,902A
FILING DATE: 07-May-1999
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 3;
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   SUITE 3200
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Pred. No. 0;
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TOPOLOGY: not relevant
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-306-902A-5
                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                            TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
STREET: 268 BUSH STREET, CITY: SAN FRANCISCO STATE: CALIFORNIA COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                         TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 94.7%;
Matches 852; Conservative 1:
                                                                      ZIP: 94104
COMPUTER READABLE FORM:
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          MAVRPGLWPVLLGIVLAAWLRGSGAQQSATVANPVPGANPDLLPHFLVEPEDVYIVKNKP
                                             VLLVCKAVPATOIFFKCNGEWVRQVDHVIERSTDGSSGEPTMEVRINVSRQQVEKVFGLE
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NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
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OF INVENTION: Netrin Receptors
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Leonardo, E. David
Hink, Lindaay
Masu, Masayuki
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Patent No. 6277585
GENERAL INFORMATION:
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US-09-306-902A-5
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CITY: SAN FRANCISCO
STATE: CALIFORNIA
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CORRESPONDENCE ADDRESS:
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US-09-306-902A-6
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/808,982
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2; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GROUP
                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Tessier-Lavigne, Marc APPLICANT: Leonardo, E. David APPLICANT: Hink, Lindsay APPLICANT: Hink, Lindsay APPLICANT: Masu, Masayuki APPLICANT: Kazuko, Keino-Masu ITTLE OF INVENTION: Netrin Receptors NUMBER OF SEQUENCES: ADDRESSEE: SCIENCE & TECHNOLOGY LAW G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 LAW (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEE: SCIENCE & TECHNOLOGY
: 268 BUSH STREET, SUITE 3
SAN FRANCISCO
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 5939271
GENERAL INFORMATION:
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NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: UC!
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Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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MOLECULE TYPE: peptide
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MEDIUM TYPE: Floppy
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USA
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STRANDEDNESS: not
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Best Local Similarity
Matches 538; Conserv
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TELEFAX: (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: SCIENCE & TECHNOLOGY LAW STREET: 268 BUSH STREET, SUITE 3200
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OF INVENTION: Netrin Receptors
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Leonardo, E. David
Hink, Lindsay
Masu, Msayuki
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REGISTRATION NUMBER: 36,627
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CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6, Application US/09306902A Patent No. 6277585 GENERAL INFORMATION:
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ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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COUNTRY:
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                                                                                                                                                                              Gaps
                                                                                                                                                                            3;
                                                                                                                                                   DB 3; Length 557;
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                                                                                                                                                   58.3%; Score 2789.5; DB 3 96.4%; Pred. No. 2.7e-256;
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APPLICANT: Leonardo, E. David
APPLICANT: Hink, Lindaay
APPLICANT: Hink, Lindaay
APPLICANT: Masu, Masayuki
APPLICANT: Kazuko, Keino-Masu
TITLE OF INVENTION: Netrin Receptors
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
                                                                                                                                                                              2; Mismatches
         INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
TYPE: amino acids
TYPE: amino acid STRANDEDNESS: not relevant
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-306-902A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 7, Application US/08808982
Patent No. 5939271
GENERAL INFORMATION:
    (415) 343-4342
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Matches 538; Conservative
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CALIFORNIA
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    TELEFAX:
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CITY: SA
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US-08-808-982-7
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52.0%; Score 2490; DB 2; Length 9
Best Local Similarity 52.3%; Pred. No. 2e-227;
Matches 496; Conservative 144; Mismatches 226; Indels
                                                                 #1.30
                                                        SOFTWARE: Patentin Recognification Version CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/808,982
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                     CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: OSWAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFREENCE/DOCKET UMBER: UC96
TELECOMMUNICATION INFORMATION:
TELECHONE: (415) 343-4341
                                                                                                                                                                                                                                                                                                                                                                                                                    SS: not relevant not relevant
                                                                                                                                                                                                                                                                                                    TELEPAX: (415) 343-4442
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERRESTICS:
LENGTH: 943 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
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MOLECULE TYPE: peptide

US-08-808-982-7
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                         HLYYCQLEASACYVFTEQLGRFALVGEALSVAAAKRLKLLLFAPVACTSLEYNIRVYCLH 673
                                         TPCYCQLEAKSCHILLDQLGTYVFTGESYSRSAVKRLQLAIFAPALCTSLEYSLRVYCLE 716
                                                                          DTHDALKEVVQLEKQLGGQLIQEPRVLHFKDSYHNLRLSIHDVPSSLWKSKLLVSYQEIP 733
                                                                                          FYHIWNGTQRYLHCTFTLERVSPSTSDLACKLWVWQVEGDGQSFSINFNITKDTRFAELL 793
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                                                                                                                                           ALESEAGVPAL--VGPSAFKIPFLIROKIISSLDPPCRRGADWRTLAQKLHLDSHLSFFA
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                                                                                                                                                                                                                                SKPSPTAMIINLWEARHFPNGNLSQLAAAVAGLGQPDAGLFTVSEAEC 899
                                                                                                                                                                                                                                               :| | | | | : | | | | | | | | : | | : | | : | : : : : : : : : | TKASPIGVILDLWEARQQDDGDLNSLASALEEMGKSEMLVAMTTDGDC 943
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALLFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: UC96-217
TELECOMMUNICATION INFORMATION:
TELEBHONE: (415) 343-4341
TELEFAX: (415) 343-4342
                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Tessier-Lavigne, Marc
Leonardo, E. David
Hink, Lindsay
Masu, Masayuki
Kazuko, Keino-Masu
TITLE OF INVENTION: Netrin Receptors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ 1D NO:
US-09-306-902A-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: not relevant TOPOLOGY: not relevant
                                                                                                                                                                                                                                                                                                                     Sequence 7, Application US/09306902A
Patent No. 6277585
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: NELT NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 94104
COMPUTER READABLE FORM:
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---DSGAQ---GLPDSFPSAPAEQLPHFLLEPEDAYIVKNKPVELHCRAF 70
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                                                                                                                      WSSSGTTKSQKAYIRIARLRKNFEQEPLAKEVSLEQGIVLPCRPPEGIPPAEVEWLRNED
                                                   PATQIFFKCNGEWVRQVDHVIERSTDGSSGEPTMEVRINVSRQQVEKVFGLEEYWCQCVA
                                                                                                                                                                                                                251 AEWSPCSNRCGRGWQKRTRTCTNPAPLNGGAFCEGQ-ACQKTACTTVCPVDGAWTEWSKW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            554 LLSPIVSCGPPGVLLTRPVILAMDHCGEPSPDSWSLRLKKQSCEGSWEQDVLHLGEEAPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DTHDALKEVVQLEKQLGGQLIQEPRVLHFKDSYHNLRLSIHDVPSSLWKSKLLVSYQEIP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TSNMTYGTFNFLGGRLMIPNTGISLLIPPDAIPRGKIYEIYLTLHKPEDVRLPLA-GCQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             614 HLYYCQLEASACYVFTEQLGRFALVGEALSVAAAKRLKLLLFAPVACTSLEYNIRVYCLH
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Patent No. 5939271
GENERAL INFORMATION:
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Leonardo, E. David
Hink, Lindsay
Masu, Masayuki
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PSLAGI-
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APPLICANT:
APPLICANT:
APPLICANT:
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609 BEAPSHLYYCQLEASACYVFTEQLGRFALVGEALSVAAAKRLKLLLFAPVACTSLEYNIR 668
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-313-288B-19
Sequence 19, Application US/08313288B
Patent No. 5750502
Patent No. 5750502
Patent No. 5750502
TITLE OF INVENTION: CLONING, EXPRESSION AND USES OF A TITLE OF INVENTION: NOVEL SECRETED PROTEIN, F-SPONDIN NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          669 VYCLHDTHDALKEVVQLEKQLGGQLIQEPRVLHFKDSYHNL 709
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

SOFTWARE: Patentin Release #1.0, Version #1.30

CURSTRICATION NUMBER: US/08/313,288B

FILING DATE: January 5, 1995

CLASSIRICATION 1040BR 15, 1995

ATTORNEY/AGENT INFORMATION:

NAME: White John P.

REGISTRATION NUMBER: 28,678

REGISTRATION NUMBER: 28,678
                 FILING DATE: 07-May-1999
CLASSIFICATION: «Unknown»
ATTORNEY, AGENT INPORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REPERRINCE/DOCKET NUMBER: 0096-217
TELECOMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 102 amino acids
APPLICATION NUMBER: US/09/306,902A
                                                                                                                                                                                                                                                                                               TYPE: amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
;
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-306-902A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: Cooper & Dunham LLP
1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 40
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0526
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: si
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: New York
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STATE:
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COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: IBM PC compatible
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: Patentin Release #1.0, Version #1.30
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CORRESPONDENCE ADDRESSE: SCIRNCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/808,982
                                                                                                   ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP STREET: 268 BUSH STREET, SUITE 3200 CITY: SAN FRANCISCO STATE: CALIFORNIA COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Tessier-Lavigne, Marc
Leonardo, B. David
Hink, Lindsay
Masu, Masayuki
Kazuko, Kelno-Masu
TITLE OF INVENTION: Netrin Receptors
NUMBER OF SEQUENCES: 9
                                   Netrin Receptors
                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-306-902A-8; Sequence 8, Application US/09306902A; Patent No. 6277585; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
       APPLICANT: Kazuko, Keino-Masu
TITLE OF INVENTION: Netrin Red
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: UC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
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CLASSIFICATION: 530
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STRANDEDNESS: not
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ZIP: 94104
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MOLECULE TYPE: peptide
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CARRIER: DNA COMPLEXES CONTAINING DNA
NVENTION: ENCODING ANTI-ANGIOGENIC PEPTIDES AND THEIR USE IN GENE
NVENTION: THERAPY
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                                                                                                                                                           SCINPAPLNGGAFCEGONVHDRTVSSLLVSVDGSWSPWSKWSACGLDCT---HWRSRECS 324
                                                                                                                                                                                    463 LCNSPVPQMGGRNCKGSGRETKACQGAPCPIDGRWSPWSPWSACTVTCAGGIRERTRVCN 522
                                                                                                                                                                                                                     DPAPRNGGEECQGTDLDTRNCTSDLCVHSASGPEDVALYVGLIAVAVCLVLLLLVLILVY 384
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                                                                                           209 RQARLADTANYTCVAKNIVARRSASAA-VIVYVNGGWSTWTEWSVCSASCGRGWQKRSR
                                                                                                                     403 QRGRSCDVISNICLGPSIQTRACSLSKCDTRIRQDGGWSHWSPWSSCSVICGVGNITRIR
                                                                     Gaps
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25.9%; Pred. No. 9e-15;
tive 35; Mismatches 114; Indels 100;
                             5.7%; Score 273.5; DB 1; Length 1172; 28.9%; Pred. No. 2.1e-16; Live 27; Mismatches 110; Indels 45;
                                                                                                                                                                                                                                                                                      385 CRKKEGLDSDVADSSILTSGFQPVSI--KPSKADNPHLLTIQPDLSTTT-
                                                                                                                                                                                                                                                      SPEPQYGGKACVGDVQERQMCNKRSC----PVDGCLSNPCFPGAQC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3: Connolly, Bove, Lodge, & Hutz
1220 Market Street, P.O. Box 2207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/608,845
FILING DATE: 16-UUL-1996
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/985,526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3, Application US/08985526
Patent No. 6080728
GENERAL INFORMATION:
APPLICANT: Mixson, James A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: McMorrow Jr., Robert G
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: Floppy disk
IBM PC compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (302) 658-5613
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 441 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 25.9%
                                                              Conservative
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MEDIUM TYPE: Floppy
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TITLE OF INVENTION:
TITLE OF INVENTION:
INUMBER OF SEQUENCES:
              Query Match
Best Local Similarity
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US-08-313-288B-19
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192 NGGWGPWSPWDICSVTCGGGVOKRSRLCV---DSRMTEENKELANELR------RPP 239
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                                                                                                                                                                              174 ----EGIPPAEVEWLRNED-LVDPSLDPNVYITREHSLVVRQARLADTANYTCVAKNIVA 228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Polverini, Peter J.
APPLICANT: Good, Deborah J.
APPLICANT: Good, Deborah J.
APPLICANT: Frazier, William A.
TITLE OF INVENTION: Method and Composition for
TITLE OF INVENTION: Inhibiting Angiogenesis
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Tilton, Fallon, Lungmus & Chestnut
STREET: 100 South Wacker Drive, Suite 960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/841,656
FILING DATE: 24-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/464,369
FILING DATE: 12-JAN-1990
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Fentress, Susan B.
REGISTRATION NUMBER: 31,327
REFERENCE/DOCKET NUMBER: 92005-PCT
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                 240 LCYHNG----VQYRNNEEWTVDSCTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PCT/US93/01652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 60606-4002
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/M9-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application PC/TUS9301652 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (312) - 456 - 8000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         i: 239 amino acids
AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bouck, Noel P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PC
                                                                                                                                                                                                                                                                                    229 RRRSASAAVIVYVNG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19930222
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512 VQKRSRLCNNPTPQFGGKDCVGDVTENQICNKQDC 546

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James A
CARRIER: DNA COMPLEXES CONTAINING DNA
ENCODING ANTI-ANGIOGENIC PEPTIDES AND THEIR USE IN GENE
THERAPY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        300 GSWSPWSKWSACGLDC---THWRSRECSDPAPRNGGEECQGTDLDTRNCTSDLC-VHSAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13;
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US-09-540-245A-15
Sequence 15, Application US/09540245A
Septence 15, Application US/09540245A
GENERAL INFORMATION:
APPLICANT: Goodman. Corey
APPLICANT: Brose, Katja
APPLICANT: Tessier-Lavigne, Marc
TITLE OF INVENTION: Modulating Robo: Ligand Interactions; FILE REFERENCE: B98-031-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , 3e-14;
nes 46;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 3;
                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Connolly, Bove, Lodge, & Hutz
STREET: 1220 Market Street, P.O. Box 2207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4.9%; Score 235.5;
38.5%; Pred. No. 5.3e
tive 16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/540,245A
                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 19899
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 18M PC compatible
COMPUTER: 18M PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/608,845
FILING DATE: 16-UUL-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                         Sequence 1, Application US/08985526
Patent No. 6080728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: MCMOITOW Jr., Robert G
TELECOMMUNICATION INFORMATION:
TELEPHONE: (302) 658-9141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (302) 658-5613
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 218 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 38.5
Matches 47; Conservative
                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Connolly,
                                                                                                                                                                                                      TITLE OF INVENTION: C
TITLE OF INVENTION: B
TITLE OF INVENTION: T
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                           CITY: Wilmington STATE: Delaware
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                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Mixson
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                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-985-526-1
                                                                                             US-08-985-526-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      452 GDGVITRIRLCNSPSPQMNGKPCEGEARETKACKKDACPINGGWGPWSPWDICSVTCGGG 511
                                                                                                                               88 IQQRGRSCDSLNNRCEGSSVQTRTCHIQECDKRFKQ-----DGGWSPWSPWSPWSSCSVTC 140
                                                                                               207 VVRQARLADTANYTCVAKNIVAR-----RRSASAAVIVYVNGGWSTWTEWSVCSASC 258
                                                                                                                                                                                      259 GRGWOKRSRSCTNPAPLNGGAFCEGONVHDRTVSSLLVSVDGSWSPWSKWSACGLDC--- 315
                                                                                                                                                                                                                              141 GDGVITRIRICNSPSPQMNGLPCEGEARETKACKKDACPINGGWGPWSPWDICSVTCGGG 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 207 VVRQARLADTANYTCVAKNIVAR-----RRSASAAVIVYVNGGWSTWTEWSVCSASC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          399 IQQRGRSCDSLNNRCEGSSVQTRTCHIQECDKRFKQ-----DGGWSHWSPWSSCSVTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18; Gaps
                                                  18; Gaps
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    Length 239;
5.1%; Score 246; DB 5; Length 23: 31.0%; Pred. No. 6.2e-15; cive 23; Mismatches 66; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thomas M. and Avihu Klar
CLONING, EXPRESSION AND USES OF A
NOVEL SECRETED PROTEIN, F-SPONDIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRING STEER.

SOFTWARE PATENTIN Release #1.0, Version #1.30
CURRINT APPLICATION DATA:
APPLICATION NUMBER: US/08/313,288B
FILING DATE: January 5, 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REGISTRATION NUMBER: 28,678
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAM: (212) 278-0400
TELEFRAM: (212) 391-0526
TELEFRAM: (212) 391-0526
TELEFRAM: (212) 391-0526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  316 THWRSRECSDPAPRNGGEECQGTDLDTRNCTSDLC 350
                                                                                                                                                                                                                                                                                                           201 VOKRSRLCNNPAPQFGGLDCVGDVTENQICNKQDC 235
                                                                                                                                                                                                                                                                              316 THWRSRECSDPAPRNGGEECQGTDLDTRNCTSDLC 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Jessell, Thomas M. and Avih
TITLE OF INVENTION: CLONING, EXPRESSIG
TITLE OF INVENTION: NOVEL SECRETED PRO
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: COOPER & LUTHAM LLP
STREET: 1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 20, Application US/08313288B Patent No. 5750502
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1170 amino acids
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                                                  48; Conservative
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MOLECULE TYPE: peptide

US-08-313-288B-20
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
    Query Match
Best Local Similarity
Matches 48; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: New York
STATE: New York
COUNTRY: USA
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STRANDEDNESS:
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Matches
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EPTME-----VRINVSRQQVEKVFGLEEYWCQCVAWSSSGTTKSQKAYIR1ARLRKNFE 152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DFPPRIVEHPSDLIVSKGEPATLNCKAEGRPTPTI-----EWYKGGERVETDKDDPRSH 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QEPLAKEVSLEQGIVLPCRPPEGIPPAEVEWLRNEDLVDPSLDPNVYIT-REHSLVVRQA 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     231 RKSDAGKYVCVGTNMVGERESEVAELTVLERPSFVKRPSNLAVTVDDSAEFKCEA---RG 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---RSRSCINPAPLNGGAFCEGQNVHDRTVSSLLV 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                288 DPVPTVRWRKDDGELPKSRYEIRDDHTLKIRKVT--AGDMGSYTCVAENMVGKAEASATL 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SVDGS----WSPWSKWSACGLDCTHWRSRECSDPAP----RNGGEEC-----QGTDL 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               346 TVQEPPHFVVKPRDQVVALGRTVT-FQCEATGNPQPAIFWRREGSQNLLFSYQPPQSSSR 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41 DLLPHFLVEPEDVYIVKNKPVLLVCKAV--PATQIFFKCNGEWVRQVDHVIERSTDGSSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RLADTANYTCVAKNIVARRRSASAAVIVYVNGGW-----STWTEWSV---CSASCGRG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----OLTNGHL---LSPLGG-GRHTLHHSSPTSEAEEFVSRLSTQNYFRSLPRGTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LTSGFQPVSIKPSKADNPHLLTIQPDLSTTTTYQGSL---CPRQDGPSPKF-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1651;
                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Brose, Katja
APPLICANT: Brose, Katja
APPLICANT: Tessier-Lavigne, Marc
TITLE OF INVENTION: Modulating Robo: Ligand Interactions
FILE REPERENCE: B98-031-3
CURRENT APPLICATION NUMBER: US/09/540,245A
CURRENT FILING DATE: 2000-03-31
PRIOR FILING DATE: 1997-11-14
PRIOR APPLICATION NUMBER: 60/065,544
PRIOR FILING DATE: 1997-11-14
PRIOR FILING DATE: 1998-04-07
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NOS: 20
TOWNER OF SEQ ID NOS: 20
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4.5%; Score 216.5; DB 3;
Best Local Similarity 20.7%; Pred. No. 1e-10;
Matches 213; Conservative 139; Mismatches 381;
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                                                                                                                                                                                                                                                                                                             ; Sequence 18, Application US/09540245A; Patent No. 6270984; GENERAL INFORMATION:
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PSN---SKTALTYEDVP
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Kid, Thomas
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ORGANISM: human
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                    Length 1395;
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4.9%; Score 234; DB 3; Lo
Best Local Similarity 20.5%; Pred. No. 1.6e-12;
Matches 188; Conservative 103; Mismatches 262;
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CURRENT FILING DATE: 2000-03-31
PRIOR PAPLICATION NUMBER: 60/065,544
PRIOR FILING DATE: 1997-11-14
PRIOR APPLICATION NUMBER: 60/081,057
PRIOR FILING DATE: 1998-04-07
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PATENTN VET. 2.0
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ORGANISM: Drosophila melanogaster
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497 535 548 548	608 625 656 682	716 728 768 785	818 844 859	88 9 8 9 8 9 8 9
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Search completed: October 4, 2004, 18:33:20 Job time: 38 secs

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October 4, 2004, 18:29:07; Search time 66 Seconds (without alignments) 4383.295 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	Sequence 2, Appli	7	7	Sequence 5, Appli	13	5,	16	1. 7	Н	6.9	9	15,	35,	121	117, 1
		ID	US-09-970-944-2	US-09-918-779-2	US-10-624-932-2	US-09-933-261-5	US-09-970-944-13	US-10-256-702-5	US-10-240-154-16	US-10-311-623-1	US-09-970-944-14	US-09-933-261-6	US-10-256-702-6	US-09-970-944-15	US-10-087-684-35	US-09-972-211-121	US-10-037-417-117
		DB	11	12	16	10	11	14	14	16	11	10	14	11	12	12	12
		Match Length	899	898	868	898	898	868	898	842	544	557	557	931	931	931	931
de	Query	Match	100.0	98.2	98.2	95.0	95.0	95.0	95.0	91.5	58.9	58.3	58.3	56.5	56.5	56.5	56.5
		Score	4787	4698.5	4698.5	4545.5	4545.5	4545.5	4545.5	4379.5	2819	2789.5	2789.5	2705.5	2705.5	2705.5	2705.5
	Result	No.	H	7	ю	4	S	9	7	8	6	10	11	12	13	14	15

	Sequence 17, Appl. Sequence 36, Appl. Sequence 36, Appl. Sequence 122, App. Sequence 119, App. Sequence 119, App. Sequence 34, Appl. Sequence 34, Appl.		
US-10-096-625-121 US-10-218-779-35 US-09-970-944-16 US-09-972-211-125 US-10-096-625-125 US-10-039-447-120	US-10-087-684-36 US-10-018-779-36 US-10-018-779-36 US-10-037-417-118 US-10-037-417-119 US-10-086-625-122 US-10-087-684-34 US-10-028-684-34	US-09-972-211-124 US-10-096-625-124 US-10-096-625-124 US-10-081-684-33 US-10-218-779-33 US-10-218-779-33 US-10-096-625-123 US-10-096-625-123 US-09-977-211-56	US-10-096-625-56 US-09-33-261-7 US-10-26-702-7 US-10-087-684-2 US-10-218-779-2 US-10-218-779-2
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## ALIGNMENTS

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Sequence 2, Application US/09970944
Publication No. US20030204052A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Rastelli, luca
APPLICANT: Rastelli, luca
APPLICANT: Shimkers, Richard A
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
Antibodies Directed Against these Proteins
TITLE OF INVENTION NUMBER: US/09/970,944
CURRENT APPLICATION NUMBER: 60/237,862
PRIOR APPLICATION NUMBER: 60/237,862
PRIOR PLING DATE: 2000-10-04
NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 899
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                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
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APPLICANT: Smithson, Glennda
TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encc
FILE REFERENCE: 21402-074 US
CURRENT APPLICATION NUMBER: US/09/918,779
CURRENT FILING DATE: 2001-07-30
FRIOR PILING DATE: 2000-07-28
FRIOR FILING DATE: 2000-08-04
FRIOR APPLICATION NUMBER: 60/223,752
FRIOR FILING DATE: 2000-08-08
FRIOR FILING DATE: 2000-08-08
FRIOR FILING DATE: 2000-08-08
FRIOR APPLICATION NUMBER: 60/223,762
FRIOR FILING DATE: 2000-08-08
FRIOR RELING DATE: 2000-08-08
FRIOR APPLICATION NUMBER: 60/223,769
FRIOR FILING DATE: 2000-08-18
FRIOR APPLICATION NUMBER: 60/225,146
FRIOR APPLICATION NUMBER: 60/225,929
FRIOR FILING DATE: 2000-08-15
FRIOR APPLICATION NUMBER: 60/225,697
FRIOR APPLICATION NUMBER: 60/225,697
FRIOR FILING DATE: 2000-08-15
FRIOR APPLICATION NUMBER: 60/225,697
FRIOR FILING DATE: 2000-08-15
FRIOR APPLICATION NUMBER: 60/225,697
FRIOR FILING DATE: 2000-08-15
FRIOR FILING DATE: 2001-02-01
FRIOR FILING DATE: 2000-08-15
FRIOR FILING FRIOR DATE: 2001-08-16
FRIOR FRIOR FRIOR DATE: 2000-08-16
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FRIOR FRIOR DATE: 20
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98.7%; Pred. No. 0;
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Matches 888; Conser
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                                                              SWSPWSKWSACGLDCTHWRSRECSDPAPRNGGEECQGTDLDTRNCTSDLCVHSASGPEDV
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                                       VEWLRNEDL VDPSLDPNVY I TREHSLVVRQARLADTANYTCVAKNI VARRRSASAAVI VY
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APPLICANT: Taupier, Raymond
APPLICANT: Padigaru, Muralidhara
APPLICANT: Rastelli, Luca
APPLICANT: Shamkets, Richard
APPLICANT: Shamkets, Richard
APPLICANT: Serhusen, Bryan
APPLICANT: Shenoy, Suresh
APPLICANT: Li, Li
APPLICANT: Li, Li
APPLICANT: Li, Li
APPLICANT: Alsobrook, John
APPLICANT: Lepley, Denise
APPLICANT: Lepley, Denise
APPLICANT: Garlach, Valerie
APPLICANT: Garlach, Valerie
APPLICANT: Garlach, Valerie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/09918779
Publication No. US20030064369A1
GENERAL INFORMATION:
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PRIOR FILING DATE: 2000-08-15
PRIOR APPLICATION NUMBER: 60/225,470
PRIOR FILING DATE: 2000-08-15
Remaining Prior Application data removed - 8
NUMBER OF SEQ ID NOS: 61
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2:
LENGTH: 898
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Best Local Similarity 98.7%;
Matches 888; Conservative
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ORGANISM: Homo sapiens
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APPLICANT: Schusen, Bryan
APPLICANT: Serbusen, Bryan
APPLICANT: Spreek, Kimberly
APPLICANT: Gress, William
APPLICANT: Gress, William
APPLICANT: Lepley, Denise
APPLICANT: Lepley, Denise
APPLICANT: Burgess, Catherine
APPLICANT: Schoe, David
APPLICANTON NUMBER: 60/222, 409
PRIOR PILING DATE: 2000-08-08
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PAPLICANT: Padigaru, Muralidhara
APPLICANT: Rastelli, Luca
APPLICANT: Spaderna, Steven
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APPLICANT: Herman, John L. APPLICANT: Herman, John L. APPLICANT: Raseelli, Luca APPLICANT: Shimkets, Richard A APPLICANT: Shimkets, Richard A TITLE OF INVENTION: No. US20030204052Alel Proteins and Nucleic Acids Encoding Same TITLE OF INVENTION: Antibodies Directed Against these Proteins
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CURRENT APPLICATION NUMBER: US/09/970,944
CURRENT FILING DATE: 2002-05-02
PRIOR APPLICATION NUMBER: 60/237,862
PRIOR FILING DATE: 2000-10-04
NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin Ver: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 13, Application US/09970944; Publication No. US20030204052A1; GENERAL INFORMATION:
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Best Local Similarity
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COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFWARE: PatentIn Release #1.0, Version #1.30
    CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/09/933,261
    FILING DATE: 20-Aug-2001
    CLASSIFICATION: CUNKNOWN>
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TITLE OF INVENTION: Netrin Receptors
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: SCB BUGSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
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94.7%; Pred. No. 0;
cive 19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 08/808,982
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REFERENCE/DOCKET NUMBER: 36,627
REFERENCE/DOCKET NUMBER: UC96-217
TELECOMMUNICATION:
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SEQUENCE DESCRIPTION: SEQ ID NO: 5:
                                                                                                                                                                                  Marc
                                                                                                                                                                                             Leonardo, E. David
Hink, Lindsay
Masu, Masayuki
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TELEFAX: (415) 343-4342
                                                                                                                      Sequence 5, Application US/09933261
Publication No. US20030040046A1
GENERAL INFORMATION:
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                                                                                                                                                                       APPLICANT: Tessier-Lavigne,
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SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 94.7%
Matches 852; Conservative
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ZIP: 94104
                                                                                                       US-09-933-261-5
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GROUP

ADDRESSEE: SCIENCE & TECHNOLOGY LAW STREET: 268 BUSH STREET, SUITE 3200 CITY: SAN FRANCISCO STATE: CALIFORNIA

Version #1.30

SOFTWARE: Patentin Release #1.0, COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS

MEDIUM TYPE: Floppy disk

COUNTRY:

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PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/933,261

FILING DATE: 20-Aug-2001

APPLICATION NUMBER: 08/808,982

FILING DATE: CHENOWN-

ATTORNEY/AGENT INFORMATION:

NAME: OSMAN, RICHARD A

REGISTRATION NUMBER: 36,627

REGISTRATION NUMBER: 36,627

TELECOMMUNICATION INFORMATION:
                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/256,702
FILING DATE: 27-Sep-2002
CLASSIFICATION: <Unknown>
                                                                      ZIP: 94104
COMPUTER READABLE FORM:
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SWSPWSKWSACGLDCTHWRSRECSDPAPRNGGEECQGTDLDTRNCTSDLCVHSASGPEDV
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Publication No. US20030059859A1
GENERAL INFORMATION:
APPLICANT: Tessier-Lavigne, Marc
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US-10-256-702-5
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TELEPHONE: (415) 343-4341 TELEFAX: (415) 343-4342

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                                                                                       US20030059859A1 Relevant
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                                       LENGTH: 898 amino acids
TYPE: amino acid
STRANDEDNESS: No. US20030059859A1 Relev
TOPOLOGY: No. US20030059859A1 Relevant
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
                                                                                                                                                                                                           tch al Similarity 94.7%; Pred. No. 0; 852; Conservative 19; Mismatches
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS
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Kazuko, Keino-Masu TITLE OF INVENTION: Netrin Receptors NUMBER OF SEQUENCES: 8 CORRESPONDENCE ADDRESS:

Leonardo, E. David Hink, Lindsay Masu, Masayuki

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300 SWSSWSKWSACGLDCTHWRSRECSDPAPRNGGEECRGADLDTRNCTSDLCLHTASCPEDV 359
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                                                                  KPEDVRLPLAGCQTLLSPIVSCGPPGVLLTRPVILAMDHCGEPSPDSWSLRLKKQSCEGS
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| Publication No. US20030175741A1
| GENERAL INFORMATION:
| APPLICANT: Cochran et al.
| TITLE OF INVENTION: SCHIZOPHRENIA RELATED GENES
| FILE REPERENCE: CKFW-P01-006
| CURRENT APPLICATION NUMBER: US/10/240,154
| CURRENT FILING DATE: 2001-04-02
| PRIOR FILING DATE: 2001-04-02
| PRIOR FILING DATE: 2001-04-02
| NUMBER OF SEQ ID NOS: 34
| SOFTWARE: Patentin version 3.2
| SEQ ID NO 16
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Best Local Similarity 94.7'
Matches 852; Conservative
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Sequence 6, Application US/09933261
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                                                                                                                                                                   EYWCQCVAWSSSGTTKSQKAYIRIARLRKNFEQEPLAKEVSLEQGIVLPCRPPEGIPPAE
                                                                                                                                                                                                                                                                 VEWLRNEDLVDPSLDPNVYITREHSLVVRQARLADTANYTCVAKNIVARRRSASAAVIVY
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                                                                                                                                                                                                                                                                                                                                                                                                                       SWSPWSKWSACGLDCTHWRSRECSDPAPRNGGEECQGTDLDTRNCTSDLCVHTASGPEDV
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                                                                                                                                                      MAVRPGLWPALLGIVLAAWLRGSGAQQSATVANPVPGANPDLLPHFLVEPEDVYIVKNKP
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                                                                                                                              Gaps
                                                                                                                               59;
                                                                                                        842;
                                                                                                      Length
                                                                    ID No. US20040023244A1 6052371CD1
                                                                                                                              2; Indels
                                                                                                        DB 16;
                                                                                                     Score 4379.5;
Pred. No. 0;
1; Mismatches
                                                                                                                              1;
                                                                                                        91.5%;
93.1%;
                                                                                                     Query Match
Best Local Similarity 93.1
Matches 838; Conservative
                                             FEATURE:

NAME/KEY: misc feature

OTHER INFORMATION: Incyte
US-10-311-623-1
                                    sapiens
                      TYPE: PRT
ORGANISM: Homo
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APPLICANT: Herrman, John L
APPLICANT: Rastelli, Luca
APPLICANT: Rastelli, Luca
APPLICANT: Rastelli, Luca
APPLICANT: Shinkers, Richard A
APPLICANT: Shinkers, Richard A
TITLE OF INVENTION: No. US2003024052Alel Proteins and Nucleic Acids Encoding Same i
TITLE OF INVENTION: Antibodies Directed Against these Proteins
FILE REPERBENCE: 21402-138
CURRENT APPLICATION NUMBER: US/09/970,944
CURRENT FILING DATE: 2002-05-02
PRIOR PILING DATE: 2000-10-04
NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 2819; DB 11;
Pred. No. 4.2e-238;
0; Mismatches 0;
Sequence 14, Application US/09970944
Publication No. US20030204052A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58.9%;
ilarity 99.6%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
Matches 540; Conserv
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360 XDSYHNLXLSXHDVPSSLWKSKLLVSYQEIPFYHIWNGTQRYLHCTFTLERVSPSTSDLA 419
                                                                                                CKIMVMQVEGDGQSFSINFNITKDTRFAELLALESEAGVPALVGPSAFKIPFLIRQKIIS 479
                                                                                                                                                                 SLDPPCRRGADWRTLAQKLHLDSHLSFFASKPSPTAMILNLWEARHFPNGNLSQLAAAVA
                                                                 CKLWVWQVEGDGQSFSINFNITKDTRFAELLALESEAGVPALVGPSAFKIPFLIRQKIIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
STREET: SCIENCE & TECHNOLOGY LAW GROUP
STREET: SAB BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: No. US20030059859A1 Relevant
TOPOLOGY: No. US20030059859A1 Relevant
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Pred. No. 1.7e-235;
2; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 27-Sep-2002
CLASSTRICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/933,261
FILING DATE: 20-Aug-2001
APPLICATION NUMBER: 08/808,982
FILING DATE: «Unknown»
ATTORNEY/AGENT THORNAMION:
ATTORNEY/AGENT THORNAMION:
REGISTRATION NUMBER: 36,627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/10/256,702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kazuko, Keino-Masu
TITLE OF INVENTION: Netrin Receptors
NUMBER OF SEQUENCES: 8
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SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
                                                                                                                                                                                                                                                                                                                                                          Sequence 6, Application US/10256702
Publication No. US20030059859A1
GENERAL INFORMATION:
APPLICANT: Tessier-Lavigne, N
Leonardo, E. David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  343-4342
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Hink, Lindsay
Masu, Masayuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (415) 343-4
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
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ilarity 96.4%;
Conservative 2
                                                                                                                                                                                                                                                              540 GTXPAGRWLLSQCSEAEC
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Best Local Simi
Matches 538;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            404 GROPVSIKPSKADNPHLLTIQPDLS-TTTTYQGSLCPRODGPSPKFQLTNGHLLSPLGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                344 NCTSDLCVHSASGPEDVALYVGLIAVAVCLVLLLLVLILVYCRKKEGLDSDVADSSILTS
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                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/933,261
FILING DATE: 20-Aug-2001
CLASSIFICATION: <UNKNOWN>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: anino acid
STRANDEDNESS: No. US20030040046Al Relevant
TOPOLOGY: No. US20030040046Al Relevant
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
                                                                                                                                                                      ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP STREET: 268 BUSH STREET, SUITE 3200 CITY: SAN FRANCISCO STATE: CALLFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 08/808,982
FLING DATE: «Uhrhown-
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: UC96-217
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Mismatches
                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                              Kazuko, Keino-Masu
TITLE OF INVENTION: Netrin Receptors
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (415) 343-4341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 557 amino acids
                  APPLICANT: Tessier-Lavigne,
                                                       Hink, Lindsay
Masu, Masayuki
                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
                                         Leonardo,
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GENERAL INFORMATION:
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Best Local Si
Matches 538;
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APPLICANT: Edinger, Shlomit
APPLICANT: Edinger, Shlomit
APPLICANT: Edinger, Shlomit
APPLICANT: Edinger, Valerie
APPLICANT: Edinger, Valerie
APPLICANT: Ellerman, Karen
APPLICANT: MacDougall, John R
APPLICANT: Millet, Isabelle
APPLICANT: Millet, Isabelle
APPLICANT: Stone, David J
APPLICANT: Stekeres Jr, Edward S
TITLE OF INVENTION: No. US20046048245Alel Human Proteins, Polynucleotides Encoding The
FILE REFERENCE: 21402-141
CURRENT APPLICATION NUMBER: US/09/972,211
                                           558
                                                                         IPRGKIYEIYLIHKPEDVRLPLAGCQTLLSPIVSCGPPGVLLTRPVILAMDHCGEPSPD 585
                                                                                                                                                                            | ::|| |: :| || ||: :|| || BWKIQLKNQAVQGQWE-DVVVVGEENFTTPCYIQLDABACHILTENLSTYALVGQSTTKA 677
                                                                                                                                                                                                                                                          765
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                858 APQTRCHDWRWLAHKLNLDRYLNYFATKSSPTGVILDLWEAQNFPDGNLSMLAAVLEEMG 917
                                                                                                                                                     SWSLRLKKQSCEGSWEQDVLHLGEEAPSHLYYCQLEASACYVFTEQLGRFALVGEALSVA
SRLS---TQNYF-----RSLPRGT--SNMTYGTFNFLGGRLMIPNTGISLLIPPDA
                      646 AAKRLKLLLFAPVACTSLEYNIRVYCLHDTHDALKEVVQLEKQLGGQLIQEPRVLHFKDS
                                                                                                                                                                                                                                                                                                             706 YHNLRLSIHDVPSSLWKSKLLVSYQBIPFYHIWNGTQRYLHCTFTLERVSPSTSDLACKL
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PRIOR FILING DATE: 2000-10-05
PRIOR PELING DATE: 2000-10-05
PRIOR PILING DATE: 2000-10-05
PRIOR APPLICATION NUMBER: 60/238,400
PRIOR APPLICATION NUMBER: 60/238,400
PRIOR APPLICATION NUMBER: 60/238,400
PRIOR PILING DATE: 2000-10-06
PRIOR PILING DATE: 2000-10-06
PRIOR PILING DATE: 2000-10-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 121, Application US/09972211
Publication No. US20040048245A1
GENERAL INFORMATION:
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Rastelli, Luca
Malyankar, Uriel M
Grosse, William M
Alsobrook II, John P
Lepley, Denise M
Spytek, Kimberly Ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Taupier Jr, Raymond J
APPLICANT: Taupier Jr, Raymond J
APPLICANT: Burgess, Catherine E
APPLICANT: Zerhusen, Bryan D
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STWIEWSVCSASCGRGWQKRSRSCINPAPLNGGAFCEGQNVHDRIVSSLLVSVDGSWSPW 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SKWSACGLDCTHWRSRECSDPAPRNGGEECQGTDLDTRNCTSDLCVHSASGPEDVALYVG 365
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                                                                                                                                                                                          APPLICANT: Miller, Charles B.
APPLICANT: Miller, Charles B.
APPLICANT: Miller, Charles B.
TILBO FOR INVENTION: PROTIENS AND NUCLEIC ACIDS ENCODING SAME FILE REFERENCE: 21402-214 CIP
CURRENT APPLICATION NUMBER: US/10/087,684
CURRENT APPLICATION NUMBER: 60/253,834
PRIOR FILING DATE: 2000-11.29
PRIOR FILING DATE: 2000-11.29
PRIOR PLING DATE: 2000-11.25
PRIOR PLING DATE: 2001-01.25
PRIOR PLING DATE: 2001-03.08
PRIOR PLING DATE: 2001-05.09
PRIOR PLING DATE: 2001-05.00
PRIOR PRILNG DATE: 2001-05.00
PRIOR PRILNG DATE: 2001-05.00
PRIOR PRILNG DATE: 2001-10-05
NUMBER OF SEQ ID NOS: 220
SOFTWARE: CuraSequist version 0.1
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            ы, ы
Padigaru, Muralidhara
                                           Mishra, Vishnu
Shenoy, Suresh G.
Rastelli, Luca
Tchernev, Velizar T.
                                                                                                                       Vernet, Corine A.M.
Zerhusen, Bryan D.
Malyankar, Uriel M.
                                                                                                                                                                                  Guo, Xiaojia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
CRGANISM: Mus musculus
US-10-087-684-35
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APPLICANT:
APPLICANT:
APPLICANT:
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                                           APPLICANT
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PPCRRGADWRTLAQKLHLDSHLSFFASKPSPTAMILNLWEARHFPNGNLSQLAAAVAGLG 885
            619 DWKIQLKNQAVQGQWE-DVVVVGEENFTTPCYIQLDAEACHILTENLSTYALVGQSTTKA 677
                                                                                                                                                                                                                                                                                                          858 APQTRGHDWRMLAHKLNLDRYLNYFATKSSPTGVILDLWEAQNFPDGNLSMLAAVLEEMG
                                                                                                                                                   738 IHNLRLSIHDIAHSLWKSKLLAKYQEIPFYHIWSGSQRNLHCTFTLERLSLNTVELVCKL
                                                                                                                                                                                                       766 WVWQVEGDGQSFSINFNITKDTRFAELLALESEAGVPALVGPSAFKIPFLIRQKIISSLD
                                                                                                                                                                                                                                798 CVRQVEGEGQIFQLNCTVSEEPTGIDLPLLDPASTITTVTGPSAFSIPLPIRQKLCSSLD
                                                  AAKRLKLLLFAPVACTSLEYNIRVYCLHDTHDALKEVVQLEKQLGGQLIQEPRVLHFKDS
                                                                                    678 AAKRLKLAIFGPLCCSSLEYSIRVYCLDDTQDALKEVLQLERQMGGQLLEEPKALHFKGS
                                                                                                                             706 YHNLRLSIHDVPSSLWKSKLLVSYQEIPFYHIWNGTQRYLHCTFTLERVSPSTSDLACKL
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APPLICANT: Miller, Charles B
APPLICANT: Eisen, Andrew J
TITLE OF INVENTION: Proteins and Nucleic Acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: 21402-235
CURRENT APPLICATION NUMBER: US/10/037,417
CURRENT APPLICATION NUMBER: US/10/037,417
CURRENT PILING DATE: 2002-09-20
PRIOR FILING DATE: 2001-01-05
PRIOR FILING DATE: 2001-01-08
PRIOR FILING DATE: 2001-01-08
PRIOR FILING DATE: 2001-02-28
PRIOR FILING DATE: 2001-02-28
PRIOR FILING DATE: 2001-02-8
PRIOR FILING DATE: 2001-02-8
PRIOR FILING DATE: 2001-02-186
PRIOR FILING DATE: 2001-05-15
PRIOR APPLICATION NUMBER: 60/291,186
PRIOR FILING DATE: 2001-05-15
PRIOR FILING DATE: 2001-05-15
PRIOR FILING DATE: 2001-05-15
PRIOR FILING DATE: 2001-05-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 117, Application US/10037417 Publication No. US20040052806Al GENERAL INFORMATION:
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APPLICATION NUMBER: 60/318,405
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Padigaru, Muralidhara
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APPLICANT: Alsobrook II, John P
APPLICANT: Tchernev, Velizar T
APPLICANT: Liu, Xiaohong
APPLICANT: Spytek, Kimberly A
APPLICANT: Grosse, William M
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Edinger, Shlomit R
Sciore, Paul
Ellerman, Karen
Malyankar, Uriel M
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Burgess, Catherine
Vernet, Corine A.M.
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Shenoy, Suresh G
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Boldog, Ferenc I
Guo, Xiaojia
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APPLICANT:
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APPLICANT:
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PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 60/238,379
PRIOR PILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 60/238,402
PRIOR PEDING DATE: 2000-10-06
PRIOR PEDING DATE: 2000-10-06
PRIOR PELING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 60/238,373
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PRIOR PILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 60/238,383
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 60/238,382
PRIOR PILING DATE: 2000-10-06
PRIOR PELING DATE: 2001-10-06
PRIOR FILING DATE: 2001-03-14
PRIOR FILING DATE: 2001-03-14
PRIOR FILING DATE: 2001-03-14
                                                                                                                                                                                                                                                                                                                                                                                             Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 198
SOFTWARE: Patentin Ver. 2
SEQ ID NO 121
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ORGANISM: Mus musculus
US-09-972-211-121
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                                                                                                                                                                                                                                                                                                                                                              Length 931;
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Best Local Similarity 56.4%; Pred. No. 9e-228;
Matches 515; Conservative 153; Mismatches 214; Indels
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/318,700
; PRIOR FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 227
; SEQ ID NO 117
; LENGTH: 931
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-037-417-117
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Db 858 APQTRGHDWRMLAHKLNLDRYLNYFATKSSPTGVILDLWBAQNFPDGNLSMLAAVLBEMG 917
Qy 886 QPDAGLFTVGEAE 898
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Db 918 RHETVVSLAAEGQ 930
Search completed: October 4, 2004, 18:34:41
Job time: 79 secs

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October 4, 2004, 18:23:31; Search time 50 Seconds (without alignments) 1729:524 Million cell updates/sec US-09-970-944-2 4787 1 MAVRPGLWPALLGIVLAAWL......AVAGLGQPDAGLFTVSEAEC 899 Title: Perfect score:

Sequence:

Scoring table:

283366 seqs, 96191526 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries seq length: 0 seq length: 2000000000 Minimum DB Maximum DB

PIR 78:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	INC. A DESCRIPTION OF STREET	-5 protein 3	enecition,	d c		7	4 -	4 ¥	andiogenesis inkih			٠,		ard minorepart			neural cell adhesi	properdin precurso	hypothetical prote		hypothetical prote	hypothetical prote	rig-1 protein - mo	hypothetical profe	Sax-3 protein - Ca	n-twrosi	hymothetical proto	icracal pr	tight junction pro	ment C6 pre
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222 VAKNIVARRRSASAAVIVYVNGGWSTWTEW-SVCSASCG----

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167.5	166	160.5	152.5	152	152	151	150	149	148.5	148	147	147	146.5	146	145.5
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## ALIGNMENTS

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N; Contains: unc-5 protein, short form
C; Species: Caenorhabditis elegans
C; Date: 30-Apr-1993 #sequence revision 28-Uul-1995 #text_change 05-Nov-1999
C; Accession: B44294
N; Leung-Hagestejin, C; Spence, A.M.; Stern, B.D.; Zhou, Y.; Su, M.W.; Hedgecock, B.M.;
A; Reference number: A44294; MIJD; 93046629; PMID: 1384987
A; Accession: B4294
A; Molecule type: DNA
A; Residues: 1.947 *cLED
A; Mote: menner: 1.947 *cLED
A; Mote: authors translated the codon CTA for residue 642 as Val; sequence shown follows
A; Mote: authors translated the codon CTA for residue 642 as Val; sequence shown follows
A; Mote: authors translated the codon CTA for residue 642 as Val; sequence shown follows
A; Mote: menner: Z21187
A; Molecule type: DNA
A; Mesidues: 1.947 *cLAT-
A; Mesidues: 1.947 *cLAT-
A; Molecule type: DNA
A; Mesidues: 1.947 *cLAT-
A; Molecule type: DNA
A; Mesidues: 1.947 *cLAT-
A; Gross-references: Extain Bristol N2; clone B0273
C; Genetics:
A; Map position: 4
A; Aintrons: 28/1; 69/3; 136/1; 170/3; 229/1; 351/2; 581/1; 886/3
C; Function:
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CCKRGNSKKSKPLKPQKMNSEKAGGIYYSEPPGVRRLLLEHQHGTLLGEKISSCSQYFEP
                               VSIKPSKADNPHLLTIQPDLSTTTTYQGSLCPRQDGPSPKFQLTNGHLLSPLGGGRHTLH
                                                    PPL-----PHSTTLR---SGKSAFSGYSSTRNAGSRAALIQECSSSSGSGGKRTMLR
                                                                                             HSSPT-SEAEEFVSRLSTQNYFRSLPRGTS-NMTYGTFNFLGGRLMIPNTGISLLIPPDA
                                                                                                                TSSSNCSDDDNYATLYDYMEDKSVLGLDTSQNIVAAQIDSNGARLSLSKSGARLIVPELA
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A,Description: required for guidance of pioneering axons and cells migrating dorsally ale C,Superfamily: unc-5 protein; immunoglobulin homology; SH3 homology; thrombospondin type C,Superfamily: unc-5 protein; immunoglobulin homology; SH3 homology; transmembrane protein; short form #status predicted <ALT>
F;30-947/Product: unc-5 protein, short form #status predicted <ALT>
F;153-2116/Domain: immunoglobulin homology <IM1>
F;153-2116/Domain: immunoglobulin homology <IM2>
F;229-300/Domain: thrombospondin type 1 repeat homology <THR2>
F;365-390/Domain: transmembrane #status predicted <TWM>
F;155-359/Domain: SH3 homology <SH3>
F;152-559/Domain: SH3 homology <SH3>
F;212-559/Domain: SH3 homology <SH3>
F;206/Binding site: carbohydrate (Asn) (covalent) #status predicted RYLHCTFTLERVSPSTSDLACKLWVWQVEGDGQSFSINFNITKDTRFAELLALESEAGVP 802 787 NGLHCSLKFRPKEINGSQFSTRVIVYQKASSTEPMVM--EVSNEPELYDATSEEREKGSV 844 31, pppmidGopcrdDbLmToEcPAolCTADSSRIVISbTAVYGSVASIFIVASFILAILAMF 388 407 448 467 498 919 265 NVSRQQVEKVFGLEEYWCQCVAWSSSG-----TTKSQKAYIRIARLRRNFEQEPLAKEVS 161 221 94 BKQLGGQLIQBPR--VLHFKDSYHNLRLSIHDV-PSSLWKSKLLVSYQEIPFYHIWNGTQ PAPRNGGEECQGTDLDTRNCTSDLCVHSASG--PEDVALYVGLIAVAVCLVLLLLVLLLV VEGEKM--LYLAVSDTLTDQPHLKPIESALSPVIVIGQCDVSMSAHDNILRRPVVVSFRH ED--GSRLLCESNDFILNEKG---NLCICIEDVIPGFSCDGPEVVBISETQHRFV---AQ SRSCTNPAPLNGGAFCEGONVHDRTVSSLLVSVDGSWSPWSKWSACGLDCTHWRSRECSD CCKRGNSKKSKPLKPQKANSEKAGGIYYSEPPGVRRLLLEHQHGTLLGEKISSCSQYFEP 408 VSIKPSKADNPHLLTIQPDLSTTTTYQGSLCPRQDGPSPKFQLTNGHLLSPLGGGRHTLH 468 HSSPT-SEABEFVSRLSTQNYFRSLPRGTS-NMTYGTFNFLGGRLMIPNTGISLLIPPDA 499 TSSSNCSDDDNYATLYDYMEDKSVLGLDTSQNIVAAQIDSNGARLSLSKSGARLIVPELA 526 IPRGKIYEIYLTLHKPEDVRLPLAGCOTLLSPIVSCGPPGV-----LLTRPVILAMDH EQLGRFALVGEAL -- SVAAAKRLKLLLFAPVACTSLE--YNIRVYCLHDTHDALKEVVQL --SILTSGFQP EPEDVYIVKNKPVLLVCKAVPATQIFFKCNGEWVRQVDHVIER--STDGSSGEPTMEVRI LEQGIVLPCRPPEGIPPAEVEWLRNEDLVDPSLDPNVYITREHSLVVRQARLADTANYTC Length 947; CGEPSP-DSWSLRLKKQSCEGSWEQDVLHLGEEAPSHLYYCQLEASA-Indels VAKNIVARRESASAAVIVYVNGGWSTWTEW-SVCSASCG-Query Match
Best Local Similarity 28.5%; Pred. No. 1.7e-61;
Matches 265; Conservative 165; Mismatches 375; YCR-----KKEGLDSDVADS-----

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A;Note: sequence extracted from NCBI backbone (NCBIN:95091, NCBIP:95096)
C;Genetics:
A;Note: sequence extracted from NCBI backbone (NCBIN:95091, NCBIP:95096)
C;Genetics:
A;Gene: GDB:THBS2; TSP2
A;Cross-references: GDB:128789; OMIM:188061
A;Map position: 6q27-6q27
C;Complex: homotrimer, disulfide linked
C;Function:
A;Description: participates in cell migration and adhesion, and in platelet aggregation
C;Superfamily: thrombospondin 1; EGF homology; thrombospondin type 1 repeat homology; vo
C;Keywords: beta-hydroxyasparagine; calcium binding; cell adhesion; glycoprotein; trimer
C;Superfamily: beta-hydroxyasparagine; calcium binding; cell adhesion; glycoprotein; trimer
C;Superfamily: homobospondin 2 #status predicted AMT>
F;19-1172/Product: thrombospondin type 1 repeat homology <THR1>
F;380-431/Domain: thrombospondin type 1 repeat homology <THR1>
F;380-431/Domain: thrombospondin type 1 repeat homology <THR3>
F;380-492/Domain: EGF homology <EGF1>
F;582-691/Domain: EGF homology <EGF1>
F;582-691/Domain: EGF homology <EGF2>
F;582-8930/Regiton: cell attechment (R-G-D) motif
F;151,316,330,457,584,710,1069/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;167-226/Disulfide bonds: interchain #status predicted
F;612/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted
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A;Molecule type: mucleic acid
A;Rosidues: 1-172 < LLAH
A;Residues: 1-172 < LLAH
A;Cross-references: GB:L0'803; GB:M87275; NID:9340421; PIDN:AAA53064.1; PID:9567241
A;Note: sequence extracted from NCBI backbone (NCBIP:81502)
A;Note: sequence extracted from NCBI backbone (NCBIP:81502)
B;Bornstein, P; O'Rourke, K; Wikstrom, K:; Wolf, F.W.; Katz, R.; Li, P.; Dixit, V.M.
B;Di. Biol. Chem. 266, 12821-12824, 1991
A;Fitle: A second, expressed thrombospondin gene (Thbs2) exists in the mouse genome.
A;Reference number: A39851; MUID:91302287; PMID:1712771
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            324
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             565 -----SSFPDGS-WSCGFCFVGFLGNGTHCEDLDECALVPDICFSTSKVPRCVNTQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          209 ROARLADTANYTCVAKNIVARRRSASAA-VIVYVNGGWSTWTEWSVCSASCGRGWQKRSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           268 SCINPAPLNGGAFCEGQNVHDRIVSSLLVSVDGSWSPWSKWSACGLDCT---HWRSRECS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            463 LCNSPVPOMGGKNCKGSGRETKACQGAPCPIDGRWSPWSPWSACTVTCAGGIRBRTRVCN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         523 SPEPQYGGKACVGDVQERQMCNKRSC-----PVDGCLSNPCFPGAQC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          45;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            / Match S.7%; Score 273.5; DB 1; Length Local Similarity 28.9%; Pred. No. 1.3e-11; les 74; Conservative 27; Mismatches 110; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        435 GSLC----PRODGPSP 446
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                                                               A;Cross-references: GB:M81339
A;Experimental source: fibroblast
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                                                                                                                                                                                                                                                                                                                                                                                                                                         brain-specific angiogenesis inhibitor 1 - human
NAlternate names: BAII protein
C;Alternate names: BAII protein
C;Species (man)
C;Date: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 12-Feb-1999
C;Accession: T00026
R;Nishimoni, H; Shiratsuchi, T; Urano, T; Kimura, Y; Kiyono, K; Tatsumi, K; Yoshid submitted to the EMBL Data Library, June 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     thrombospondin 2 precursor - human ("Species: Homo sapiens (man) ("Species: Homo sapiens (man) ("Species: Homo sapiens (man) ("Species: Homo sapiens (man) ("Spaces: Homo sapiens ("Another to "B. "A47179; A42173 ("Spaces: "A47779; A47179; A42173 ("Spaces: "A77779; A77779; A77779
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ALVGPSAFKIPFLIRQKIISSLDPPCRRGADWRTLAQKLHLDSHLSFFASKP--SPTAMI 860
                                              : |::|| :: :: || | :| :| || CV----EFRLPFGVKDELARLLDMPNESHSDWRGLAKKLHYDRYLQFFASFPDCSPTSLL 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CNREACGPAGRISSRSQSLRSTDARR---REELGDEL---QOFGFPA-POTGDPAAE-EW 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              361 --SPWSVCSSTCGEGWQTR-----TRFCVSSSYSTQCSGPLREQRLCNNSAVCPVHG 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GWSTWTEWSVCSASCGRGWQKRSRSCTNPAPLNGGAFCEGQNVHDRTVSSLLV---SVDG 300
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411 AWDEWSPWSICGSTCGRGFRDRITRICR--PPQFGGNPCEGPERQIKFCNIALCPGRAVDG 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                124 COCVAWSSSGTIKSOKAYIRIARLRKNFEQEPLAKEVSLEGGIVLPCRPPEGIPPAEVEW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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A;Residues: 1-1172 <LAB>
A;Cross-references: GB:LL2350; NID:g307505; PIDN:AAA03703.1; PID:g307506
R;LaBell, T.L.; Milewicz, D.J.; Disteche, C.M.; Byers, P.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SWSPWSKWSACGLDCT -- - HWRSRECSDPAPRNGGEECQGTDLDTRNCTSDLC 350
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C;Superfamily: thrombospondin type 1 repeat homology
F;408-462/Domain: thrombospondin type 1 repeat homology <THR3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: EMBL:AB005297; NID:d1175078; PID:d1024528
A;Experimental source: brain
                                                                                                                                                             861 LNLWEARHFPNGN-LSQLAAAVAGLGQPDA 889
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|IDLWEASSSGSARAVPDLLQTLRVMGRPDA 930
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A;Molecule type: mRNA
A;Residues: 1-1584 <NIS>
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A; Title: Thrombospondin II:
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A, Molecule type: mRNA
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                                                                                845
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cell

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55; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Experimental source: brain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Substituting precursor - human c; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 10-Apr.1998 #sequence_revision 08-May-1998 #text_change 17-Nov-2000
C; Accession: JCS928
R; Simmons, A.D.; Pueschel, A.W.; McPherson, J.D.; Overhauser, J.; Lovett, M.
Biochem: Biochem: 242, 685-631, 1998
A; Tille: Molecular cloning and mapping of human semaphorin F from the Cri-du-chat candid A; Reference number: JCS928, MUID:9812554; PMID:9464278
A; Reference number: JCS928
A; Status: nucleic acid sequence not shown
A; Molecule type: mRNA
A; Residues: 1-1074 &SIM>
A; Cross-references: GB:U52840; NID:g2772583; PIDN:AAC09473.1; PID:g2772584
A; Residues: 1-1074 &SIM>
A; Cross-references: GB:U52840; NID:g2772583; PIDN:AAC09473.1; PID:g2772584
A; Residues: 1-1074 &SIM>
A; Cross-references: GB:U52840; NID:g2772583; PIDN:AAC09473.1; PID:g2772584
A; Residues: 1-1074 &SIM>
A; Cross-references: GB:U52840; NID:g2772583; PIDN:AAC09473.1; PID:g2772584
A; Residues: 1-1074 &SIM>
A; Cross-references: Brain
C; Comment: This protein disrupts normal brain development and leads to some of the featu C; Genericies:
A; Gene: semaf
C; Comment: Signal sequence #status predicted <SIM>
F; 1-20/Domain: semaphorin #status predicted <SIM>
F; 971-993/Domain: thrombospondin type 1 repeat homology <FHR3>
F; 971-993/Domain: transmembrane #status predicted <TMM>
F; 971-993/Domain: transmembrane #status predicted <TMM>
                  Anolecule type: mRNA
A, Residues: 1-873 «BOR»
A, Residues: 1-873 «BOR»
A, Residues: 1-873 «BOR»
A, Cross-references: GB: M64866; NID: g201994; PIDN: AAA40432.1; PID: g201995
A, Cross-references: GB: M64866; NID: g201994; PIDN: AAA40432.1; PID: g201995
C, Superfamily: thrombospondin 1; EGF homology; thrombospondin type 1 repeat homology «VWC»
F, 319-377 / Domain: while hard factor type C repeat homology «VWC»
F, 330-431 / Domain: thrombospondin type 1 repeat homology «THR1»
F, 492 / Domain: thrombospondin type 1 repeat homology «THR2»
F, 535 - 549 / Domain: EGF homology «EGFT»
F, 553 - 588 / Domain: EGF homology «EGFT»
F, 553 - 569 / Domain: EGF homology «EGFT»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ä
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            268 SCINPAPLNGGAFCEGQNVHDRTVSSLLVSVDGSWSPWSKWSACGLDCT---HWRSRECS 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         463 LCNSPVPQMGGKNCKGSGRETKPCQRDPCPIDGRWSPWSPWSACTVTCAGGIRERSRVCN 522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           843 VWSCWSPWTKCSATCGGGHYWRTRSCSNPAPAYGGDICLGLHTEFALCNTQPCPESWS 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         301 SWSPWSKWSACGLDC---THWRSRECSDPAPRNGGEECQGTDLDTRNCTSDLCVHSAS 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein KIAA0550 - human
C;Species: Homo sapiens (man)
C;Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     209 RQARLADTANYTCVAKNIVARRRS-ASAAVIVYVNGGWSTWTEWSVCSASCGRGWQKRSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            403 QRGRSCDVTSNTCLGPSIQTRTCSLGKCDTRIRQNGGWSHWSPWSSCSVTCGVGNVTRIR
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                                                                                                                                                                                                                                                                                                                                                                                  Similarity 36.1%; Score 273.5; DB 2; Similarity 36.1%; Pred. No. 1.3e-11; 57; Conservative 22; Mismatches 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5.7%; Score 270.5; DB 2;
42.4%; Pred. No. 1.9e-11;
Niematches 52;
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preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                57;
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Best Local S
Matches 57
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R;Nagase, T.; Ishikawa, K.; Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, O. DNA Res. 5, 31-39, 1998
A;Title: Prediction of the coding sequences of unidentified human genes. IX. The complete A;Reference number: Z14086; MUID:98290545; PMID:9628581
A;Accession: T00326
A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     273
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         375 PQYGGRPCEGPETHHKPCNIALCPVDGQWQEWSSWSQCSVTCSNGTQQRSRQCT--AAAH 432
                                                                                                                                                                                                               A;Molecule type: mRNA
A;Residues: 1-984 <NAG>
A;Cross-references: EMBL;AB011122; NID:g3043623; PIDN:BAA25476.1; PID:g3043624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               317 TCVSPYGTHCSGPLRESRVCNNTALCPVHGVWEEWSPWSLCSFTCGRGORTRTRSCT--P 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               274 PLNGGAFCEGONVHDRTVSSLLVSVDGSWSPWSKWSACGLDC---THWRSRECSDPAPRN 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           375 PQYGGRPCEGPETHHKPCNIALCPVDGQWQEWSSWSQCSVTCSNGTQQRSKQCT--AAAH 432
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A;Cross-references: EMBL:AB005299; NID:g3021700; PIDN:BAA25363.1; PID:g3021701
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          220 TCVA-----KNIVARRSASAAVIVYVNGGWSTWTEWSVCSASCGRGWOKRSRSCTNPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drain-specific angiogenesis inhibitor 3 - human
NyAlternate names: BAI3 protein
Cispecies: Homo sapiens (man)
Cispecies: Homo sapiens (man)
Cispecies: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 21-J
Cispecies: Nishimori, H.; Ichise, H.; Nakamura, Y.; Tokino,
Cytogenet. Cell Genet. 79, 103-108, 1997
A;Title: Cloning and characterization of BAI2 and BAI3, novel genes
A;Reference number: 214066; MUID:98194217; PMID:9533023
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5.6%; Score 267.5; DB 2; Length 984; ilarity 37.7%; Pred. No. 2.8e-11; Conservative 22; Mismatches 54; Indels 15;
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A,Map position: 6q12-6q12
C,Superfamily: thrombospondin type 1 repeat homology
F,344-398/Domain: thrombospondin type 1 repeat homology <THR3>
                                                                                                                                                                                                                                                                                                                                                                  A;Note: KIAA0550
C;Superfamily: thrombospondin type 1 repeat homology
F;344-398/Domain: thrombospondin type 1 repeat homology <THR3>
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37.7%; Pred. No. 5.1e-11;
tive 22; Mismatches 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        331 GGEECOGIDIDIRNCISDLCVHSASG 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGEECQGTDLDTRNCTSDLCVHSASG 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Accession: T00028
A,Status: translated from GB/EMBL/DDBJ
A,Molecule type: mRNA
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37;

323 273

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LHFFF------LSSFCWVLTEAWQSYLAVIGRMRTRLVRKRFLCLGWGLPALVVA 1039
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                                                                                                                                                                                                                                                                                                                                                                                                                                        324 CVSSPYGTLCSGPLRETRPCNNSATCPVHGVWEEWGSWSLCSRSCGRGSRSRRRTCV--P 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PLNGGAFCEGONVHDRTVSSLLVSVDGSWSPWSKWSACGLDC---THWRSRECSDPAPR- 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           462 GRHTLHHSSPISEAEEFV----SRLSIQNYFRSLPRG----TSNMTYGTFN 504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   733 RRGMKDWVRHSEDRLFLPKEVLSLSSPGKPATSGAAGSPGRGRGPGTVPPGPGHSHQRLL 792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---IYE-IYLTHKPEDVRLPLAGCQTLLSPIVSCGPPGVLLTRPVIL 574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         630 BQLGRFALVGE----ALSVAAAKRLKLLLFAPVACTSLEYNIRVYCLHDTHDALKEVVQ 684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      562 QGVAYWGLPSFARCISHEYRYLYLSLREHLAKGQRMLAGEGMSQVVRS-LQELLARRTYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---ILLINFCLSI--LASNI----LILVGQSRVLSKGVCTMTAAF
                                                                                                                                                                                                                                                                                                                       271 PEEEPKVKTOWPRSAD-----EPGLYMAQTGDPAAEEWSPWSVCSLTCGQGLQVR-TRS
                                                                                                                                                                                                                                                                                                                                                                                          214 ADTANYTCVAKNIVARRRSASAAVIVYVNGGWSTWTEWSVCSASCGRGWQKRSRSCTNPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           382 POHGGKACEGPELQTKLCSMAACPVEGOWLEWGPWGPCSTSCANGTQORSRKCSVAGPAW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTGEEVKPCSEKRCPAFHEMCRDEYVMLMTWKKAAAGEIIYNKCPPNASGSASRRCLLSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           363 ----YVGLIAVAVCL---VLLLLVLILVYCRKKEGLDSDVADSSILTSGFQPVSIKPSKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -NGHLLSPLGG
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                                                                                                                                                                                                                                                            - ITREHSLVVRQARL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -PDAIPRGK---
                                                                                                                   h 5.4%; Score 258; DB 2; Length 1572;
Similarity 18.8%; Pred. No. 2.6e-10;
72; Conservative 110; Mismatches 312; Indels 322;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 416 DNPHLLTIQPDLSTTTTY-QGSLCPRQDGPSPKFQLT-----
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                                                                                                                                                                                                                                                               PEGIPPAEVEWLRNEDLVDPSLDPNVY---
                     A)Cross-references: GDB:9838089; OMIM:602683
A;Map position: 1p35-1p35
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A, Gene: GDB:BAI2
                                                                                                                                                             Best Local Sim
Matches 172;
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N;Alternate names: BAI2 protein
C;Species: Homo sapiens (man)
C;Date: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 21-Jul-2000
C;Accession: T00027
R;Shiratsuchi, T.; Nishimori, H.; Ichise, H.; Nakamura, Y.; Tokino, T.
Cycogener. Cell Genet. 79, 103-108, 1997
A;Title: Cloning and characterization of BAI2 and BAI3, novel genes homologous to b A;Reference number: 214066; MUID:98194217; PMID:9533023
A;Accession: T00027
A;Status: translated from GB/EMEL/DDBJ
A;Batus: translated from GB/EMEL/DDBJ
A;Residues: 1-1572 <SHI>A;Residues: 1-1572 <SHI>A;Experimental source: brain
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                             A, Residues: 1-1444 -WIL.
A, Cross-references: EMBL: Z50004; PIDN: CAA90293.1; GSPDB: GN00028; CESP: C02B4.1
A, Experimental source: clone C02B4
A, Experimental source: clone C02B4
S, EMMINIARY, A.
Submitted to the EMBL Data Library, July 1995
A; Reference number: Z19917
A; Accession: T24653
A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:Z50006; PIDN:CAA90302.1; GSPDB:GN00028; CESP:C02B4.1 A;Experimental source: clone T07C5
                                                                                                                       C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C;Accession: T18856; T24653
R;McMurray, A.
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5.5%; Score 263.5; DB 2; Length 1444;
Best Local Similarity 26.4%; Pred. No. 9.3e-11;
Matches 73; Conservative 26; Mismatches 91; Indels 87;
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                                                                                              angiogenesis inhibitor homolog - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                              A;Status: praliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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                                                                                                                                                                                                                                                                                                  A, Reference number: Z19031
A; Accession: T18856
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415

620 461

336 501 362 561 678

732

629

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A; Molecule type: mRNA
A; Residues: 1-1170 <LAW>
A; Residues: 1-1170 <LAW>
A; Cross-references: GB:X04665; NID:g37137; PIDN:CAA28370.1; PID:g37138
A; Orces-references: GB:X04665; NID:g37137; PIDN:CAA28370.1; PID:g37138
B; Laherty, C.D.; Gierman, T.M.; Dixit, V.M.
J. Biol. Chem. 264, 11222-11227, 1989
A; Title: Characterization of the promoter region of the human thrombospondin gene. DNA
A; Reference number: A34274; MUD:89291870; PMID:2544587
A; Residues: 1-166 <LAH>
A; Residues: 1-166 <LAH>
A; Residues: 1-166 <LAH>
A; Residues: 1-166 <LAH>
A; Cross-references: GB:J04835
A; Cross-references: GB:J04835
A; Title: Complete thrombospondin mRNA sequence includes potential regulatory sites in the A; Reference number: A30140; MUID:89139590; PMID:2918029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Mesiduces: 1-83, 42, 85-522, 44, 524-1170 <a href="https://december.1-837465">https://december.1-837465</a>
A; Mesiduces: 1-83, 42, 85-522, 47, NID: 937464; PIDN: CAA32889.1; PID: 937465
A; Note: parts of this sequence, including the amino end of the mature protein, were deters. Richosyashi, S.; Eden-McCutchan, F.; Framson, P.; Bornstein, P. Biochemistry 25, 8418-8425, 1986
Biochemistry 25, 8418-8425, 1986
A; Title: Partial amino acid sequence of human thrombospondin as determined by analysis of A; Reference number: A25812; MUID: 87157592; PMID: 303336
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A.Residues: 1-83,'A',85-374,'RC' <DIX>
A.Residues: 1-83,'A',85-374,'RC' <DIX>
A.Residues: 1-83,'A', 85-374,'RC' <DIX>
A.Rotoser-references: GB.M14326, NID:g340005; PIDN:AAA61237.1; PID:g553801
A.Note: parts of this sequence, including the amino end of the mature protein, were deterning, X.; Skorstengaard, K.; Mosher, D.F.
J. Cell Biol. 118, 693-701, 1992
A.Title: Disulfides modulate RGD-inhibitable cell adhesive activity of thrombospondin.
A.Reference number: A42927; MUID:92348511; PMID:1379247
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A;Note: the list of introns may be incomplete
C;Complex: homotrimer, disulfide linked
C;Complex: homotrimer, disulfide linked
C;Punction:
A;Description: participates in cell migration and adhesion, and in platelet aggregation
C;Csuperfamily: thrombospondin 1; EGF homology; thrombospondin type 1 repeat homology; vo
C;Keywords: beta-hydroxyasparagine; calcium binding; cell adhesion; glycoprotein; trimer
F;1-18/Domain: signal sequence #status predicted <SIG>F;39-10/Product: thrombospondin 1 #status predicted +MAT>
F;3178-429/Domain: thrombospondin type 1 repeat homology <THR1>
F;4314-490/Domain: thrombospondin type 1 repeat homology <THR2>
F;441-547/Domain: thrombospondin type 1 repeat homology <THR2>
F;441-547/Domain: prome homology in type 1 repeat homology <THR3>
CiSpecies: Howo sapients of minimal (Species: Howo sapients) indicated (Species: Howo sapients) indicated (Species: Howo sapients) indicated (Spaces: 13-Aug-1987 #sequence_revision 03-Aug-1995 #text_change 17-Nov-2000 CiAccesion: A26155; A34274; A30140; A25812; A05172; A42927 R; A42927 R.O. J. Cell Biol. 103, 1635-1648, 1986
J. Cell Biol. 103, 1635-1648, 1986
A; Title: The structure of human thrombospondin, an adhesive glycoprotein with multiple A; Reference number: A26155; MUID:87057617; PMID:2430973
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A; Residues: 1-83, 'A', 85-397 < KOB>
A; Cross-references: GBNS631, NID:9538353; PIDN:AAA36741.1; PID:9538354
R; Dixit, V.M.; Hennessy, S.W.; Grant, G.A.; Rotwein, P.; Frazier, W.A.
Proc. Natl. Acad. Sci. U.S.A. 83, 5449-5453, 1986
A; Reference number: A05172; MUID:86287276; PMID:3461443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: protein
A;Residues: 987-1003 <SUN>
A;Note: Cys-992 is shown to have a free sulfhydryl
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A)Cross-references: GDB:120438; OMIM:188060
A)Map position: 15q15-15q15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: A25812
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                                                                                                                                                                                                                                                                                                                                                                                                                            A: Title: Expression and initial characterization of recombinant mouse thrombospondin 1 d.; Reference number: S68787; MUID: 96234006; PMID: 8654563
A; Recession: S68787
A; Recession: S68787
A; Molecule type: protein
A; Residues: 19-26, 7X, 28-37 cCHE
C; Complex: homotrimer, disulfide linked
C; Superfamily: thrombospondin 1; EGF homology; thrombospondin type 1 repeat homology; vc
C; Superfamily: thrombospondin 1; EGF homology; thrombospondin type 1 repeat homology; vc
C; Superfamils: signal sequence #status predicted <NG>
F; 1-18 / Domain: signal sequence #status predicted <NG>
F; 1-10 / Product: thrombospondin 1 #status predicted <NG>
F; 1-10 / Product: thrombospondin type 1 repeat homology <THR1>
F; 1-11 / Opmain: thrombospondin type 1 repeat homology <THR1>
F; 1-11 / Opmain: EGF homology <EGF>
F; 1-12 / Opmain: EGF homology <EGF>
F; 1-12 / Opmain: Air combospondin type 1 repeat homology <THR1>
F; 1-12 / Opmain: EGF homology <EGF>
F; 1-12 / Opmain: Hirombospondin type 1 repeat homology <THR2>
F; 1-12 / Opmain: EGF homology <EGF>
F; 1-13 / Opmain: EGF homology <EGF>
F; 1-14 / Opmain: EGF homology <EGF>
F; 1-14 / Opmain: EGF homology <EGF>
F; 1-14 / Opmain: EGF homology <EGF>
F; 1-14 / Opmain: EGF homology <EGF>
F; 1-15 / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / EGF / E
                                                                      C;Species: Mus musculus (house mouse)
C;Date: 05-Jun-1992 #sequence revision 05-Jun-1992 #text_change 20-Aug-1999
C;Date: 05-Jun-1992 #sequence revision 05-Jun-1992 #text_change 20-Aug-1999
C;Accession: A40558; A37905; B42587; S68787
G;Lawler, J.; Duquette, M.; Ferro, P.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.A. Genomics 11, 587-600, 1991
A;Title: Characterization of the murine thrombospondin gene.
A;Reference number: A40558; MUID:92128941; PMID:1774063
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              259 GRGWQKRSRSCINPAPLNGGAFCEGONVHDRTVSSLLVSVDGSWSPWSKWSACGLDC--- 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             399 IQQRGRSCDSLNNRCEGSSVQTRTCHIQECDKRFKQ------DGGWSHWSPWSSCSVTC 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      512 VQRRSRLCNNPTPQFGGKDCVGDVTENQVCNKQDC-----PIDGCLSNPCFAGAKC 562
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29.9%; Pred. No. 9.5e-10;
tive 24; Mismatches 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A;Residues: 1-1152,'P',1154-1170 <LAH>
A;Cross-references: GB:M87276
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                                     thrombospondin 1 precursor
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Matches 53; Conserv
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F;551-586/Domain: EGF homology <EGFl> F;650-689/Domain: EGF homology <EGF2>

12 RESULT TSHUP1

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                                                                                                                                                                                               al Similarity
205; Conserv
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Matches
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CySpecies: Gallus gallus (chicken)
CySpecies: Gallus gallus (chicken)
CySpecies: Gallus gallus (chicken)
CyAccession: A39804
Exequence_revision 10-Sep-1999 #text_change 10-Sep-1999
CyAccession: A39804
Exidawler, J.; Duquette, M.; Ferro, P.
J. Biol. Chem. 266, 8039-80493, 1931
Ayritle: Cloning and sequencing of chicken thrombospondin.
Axritle: Cloning and sequencing of chicken thrombospondin.
Axritles: preliminary
Axritles: preliminary
Axritles: preliminary
Axritles: Presentes: GB:M60853; NID:g212763; PIDN:AAA51437.1; PID:g212764
Axresidues: 1-1178 < LAW>Axresidues: 1-1178 < LAW>Axresidues: 1-1178 < LAW>Axresidues: GB:M60853; NID:g212763; PIDN:AAA51437.1; PID:g212764
CySuperfamily: thrombospondin 1; EGF homology; thrombospondin type 1 repeat homology <VWC>
F;325-383/Domain: thrombospondin type 1 repeat homology <THR1>
F;442-498/Domain: thrombospondin type 1 repeat homology <THR2>
F;499-555/Domain: thrombospondin type 1 repeat homology <THR2>
F;658-697/Domain: EGF homology <EGF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  transmembrane receptor protein Robol - rat
C;Species: Rattus norvegicus (Norway rat)
C;Species: Co-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: T14160
R;Kidd, T.; Brose, K.; Mitchell, K.J.; Fetter, R.D.; Tessier-Lavigne, M.; Goodman, C.S.; 2611 22, 205-215, 1998
A;Title: Roundabout controls axon crossing of the CNS midline and defines a novel subfam A;Reference number: Z17897; MUID:98117249; PMID:9458045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ş
F;926-928/Region: cell attachment, colling the predicted F;171-232/bisulfide bonds: #status predicted F;248,360,708,1067/Binding site: carbohydrate (Asn) (covalent) #status predicted F;270,274/bisulfide bonds: interchain #status predicted F;270,274/bisulfide bonds: interchain #status predicted F;1051/Binding site: carbohydrate (Asn) (covalent) #status absent F;1051/Binding site: carbohydrate (Asn) (covalent) #status absent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4;
                                                                                                                                                                              3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CNSPIPOMGGKNCVGNGRETEKCEKAPCPVNGOWGPWSPWSACTVTCGGGIRERSKLCNS 529
                                                                                                                                                                                                                                                                                                    315
                                                                                                                                                                                                                      258
                                                                                                                                                                                                                                                            451
                                                                                                                                                                                                                                                                                                                                GDGVITRIRLCNSPSPQMNGKPČEGEARETKACKKDACPINGGWGPWSPWDICSVTCGGG 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CINPAPLNGGAFCEGONVHDRIVSSLLVSVDGSWSPWSKWSACGLDC---THWRSRECSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RGRSCDVTRSACTGPHIQTRMCSFKKCDHRIRQDGGWSHWSPWSSCSVTCGVGNITRIRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     210 QARLADTANYTCVAKNIVARRRS-ASAAVIVYVNGGWSTWTEWSVCSASCGRGWQKRSRS
                                                                                                                                                                                                                                                    IQQRGRSCDSLNNRCEGSSVQTRTCHIQECDKRFKQ-----DGGWSHWSPWSSCSVTC
                                                                                                                                                                                                                                                                                                    GRGWQKRSRSCINPAPLNGGAFCEGQNVHDRIVSSLLVSVDGSWSPWSKWSACGLDC---
                                                                                                                                                                                                                      207 VVRQARLADTANYTCVAKNIVAR-----RRSASAAVIVYVNGGWSTWTEWSVCSASC
                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15;
                                                                                                                                                                                18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5.1%; Score 243.5; DB 1; Length 1178;
larity 34.4%; Pred. No. 2.1e-09;
Conservative 15; Mismatches 75; Indels 15;
                                                                                                                                      Length 1170;
                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PAPRNGGEECQGTDLDT-----RNCTSDLCVHSASGP 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PEPQYGGKPCVG---DTKQHDMCNKRDCPIDGCLSNPCFP
                                                                                                                                        Score 246; DB 1;
Pred. No. 1.3e-09;
24; Mismatches 66
                                                                                                                                                                                                                                                                                                                                                                                                                        VOKRSRLCNNPTPQFGGKDCVGDVTENQICNKQDC
                                                                                                                                                                                                                                                                                                                                                                                       316 THWRSRECSDPAPRNGGEECQGTDLDTRNCTSDLC
                                                                                                                                           5.1%;
                                                                                                                                                                                   47; Conservative
                                                                                                                                                                Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 55; Conserv
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function as the gatekeeper controlling midline crossing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | | | | : : | : | : : | : : | EE-RPSAPPRS--VIVSKNDGNGTAILVIWQPPPEDIQNGNVQEYKVWCLGNETRYHINK 828
A;Accession: T14160
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-1651 «XID>
A;Cross-references: EMBL:AF041082; NID:g2811215; PID:g2811216; PIDN:AAC39960.1
C;Function:
A;Description: appears to function as the gatekeeper controlling midline crossiC;Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----OLGRFALVG 639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               674
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         714
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      165 VAILRDDFRQNPSDVMVAVGEPAVMECQPPRGHPEPTISWKKDGSPLD---DKDERITIR 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                              | | : | |: | |: | DPPPRIVEHPSDLIVSKGEPATINCKAEGRPTPTIEWYKGGERV-ETDKDDPRSHRMLLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |---GASHGESEWLVFEVRTPTKNSVVIPDLRKGVNYEIKARPFFNEFQGADSEIKFAKTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----RSRSCINPAPLNGGAFCEGQNVHDRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    282 KCEARGDPVPTFGWRKDDGELPKSRYEIRDDHTLKIRKVT--AGDMGSYTCVAENMVGKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 340 BASATLIVQEPPHFVVKPRDQVVALGRTVT-FQCBATGNPQPAIFWRREGSQNLLFSYQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -QGTDLDTRNCTSDLCVHSASGPEDVALYVGLIAVAVCLVLLLLVLILVYCRKKEGLDSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VADSSILTSGFQPVSIKPSKADNPHLLTIQPDLSTTTTYQGSL---CPRQDGPSPKF---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QLTNGHL---LSPLGG-GRHTLHHSSPTSEAEEFVSRLSTQNYFRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LPRGTSNMTYGTFNFLGGRLMIPNTGISLLIP----PDAIPRGKIYEIYLTLHKPEDVRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----NVVLHLHNPTILSSSSVEV----HWTVDQQSQYIQ----GYKILYRPS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            700 LHFKDSYHNLRLSIHDVPSSLWKSKLL-----VSYQ--EIPFYHIWNGTQRYLHCTFTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             144 IARLRKNFEQEPLAKEVSLEQGIVLPCRPPEGIPPAEVEWLRNEDLVDPSLDPNVYIT-R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      222 GGKLMITYTRKSDAGKYVCVGTNMVGERESKVADVTVLERPSFVKRPSNLAVTVDDSAEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---TDGSSGEPTMEVRINVSRQQVEKVFGLEEYWCQCVAWSSSGTTKSQKAYIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EHSLVVROARLADTANYTCVAKNIVARRRSASAAVIVYVNGGW------STWTEWSV--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        291 VSSLLVSVDGS----WSPWSKWSACGLDCTHWRSRECSDPAP----RNGGEEC----
                                                                                                                                                                                                                                                                                                                                                                                                                  DLLPHFLVEPEDVYIVKNKPVLLVCKAV--PATQIFFKCNGEWVRQVDHVIERS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               621 IKGLKPNAIYLFLVRAANAYGISDPSQISDPVKTODVPPTTOGVDHKOVQRELG-
                                                                                                                                                                                                                                                                                         Length 1651;
                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                490 KDGVLVSTQDSRIKQLESGVLQIRYAKLGDTGRYTCTASTPSGEA
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                                                                                                                                                                                                                                                                                                                    1.6e-07;
                                                                                                                                                                                                                                                                                         DB 2;
                                                                                                                                                                                                                                                                                     4.6%; Score 220.5; I
larity 20.1%; Pred. No. 1.6e
Conservative 132; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POSSSRFSVSQTGDLTVTNVQ-RSDVGYY-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                124 SGSLFFLRIVHGRKSRPDEGVYI-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -CSASCGR----GWOK-----
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	OY 632 LGRFALVGBALSVAAAKTKILLFAPVACTSLEYNIRVYCHDTHDALKEVVOLEKQLGG 691  Db 634 LGNVVLHLHNFILSSSSVEVHWTVDQGSQTVQGY 668  OY 692 QLIOEPRVLHFKDSYHNLRLSIHDVPSSLWKSKLLVSYQEIPFYHIWNGTQR 743  :::	Qy 879 AAVAGLGQPDAGLFTVSE 896	Search completed: October 4, 2004, 18:32:42 Job time : 56 secs						
QY         804         LVGPSAFKIPFLIRQKIISSLDPPCRRGADWRTLAQKLHLDSH	RESULT 15 T30805 dutt1 protein - mouse Millernate names: transmembrane receptor protein Robol homolog C;Species: Mus musculus (house mouse) C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 22-Oct-1999 C;Accession: 130805 R;Wu, M.C.; Lowe, N.; Fordham, R.; Rabbitts, P. R;Dmitted to the EMBL Data Library, July 1998 R;Wu, M.C.; Lowe, N.; Fordham, R.; Rabbitts, P. A;Description: The mouse homologue of human DUTII/H-robol gene: protein sequence and chr. A;Reference number: 22879 A;Recession: T30805 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Accession: T30805 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Accession: T30805 A;Status: 2-1612 < WUM> A;Crossion: 1-1612 < WUM> A;Crossion: 2-1612 < WUM A;Crossion: 2-1612 < WUM A;Crossion: 2-1612 < WUM A;Crossion: 2-1612 < WUM A;Crossion: 2-1612 < WUM A;Crossion: 2-1612 < WUM A;Crossion: 2-1612 < WUM A;Crossion: 2-1612 < WUM A;Crossion: 2-1612 < WUM A;Crossion: 2-1612 < WUM A;Crossion: 2-1612 < WUM A;Crossion: 2-1612 < WUM A;Crossion: 2-1612 < WUM A;Crossion: 2-1612 < WUM A;Crossion: 2-1612 < WUM A;Crossion: 2-1612 < WUM A;Crossion: 2-1612 < WUM A;Crossion: 2-1612 < WUM A;Crossion: 2-1612 < WUM A;Crossion: 2-1612 < WUM A;Crossion: 2-1612 < WUM A;Crossion: 2-1612 < WUM A;Crossion: 2-1612 < WUM A;Crossio	Query Match 4.5%; Score 217.5; DB 2; Length 1612; Best Local Similarity 19.9%; Pred. No. 2.6e-07; Matches 211; Conservative 133; Mismatches 359; Indels 355; Gaps 52;	OY 41 DLLPHFLVBPEDVYIVKNKPVLLVCKAVPATQIFFKCNGEWVRQVDHVIERS 92  Db 26 DFPPRIVEHPSDLIVSKGEPATLNCKAEGRPTFTIEWYKGGERV-ETDKDDPRSHRMLLP 84	QY 93TDGSSGEPTMEVRINVSRQQVEKVFGLEEYWCQCVAWSSSGTTKSQKAYIR 143  Db 85 SGSLFFLRIVHGRKSRPDEGVXICVARNYLGEAVSHNASLE 125	144 IARLRKNFEQEPLAKEVSLEGGIVLPCRPPEGIPPAEVEWLRNEDLVDPS	QY 203 EHGLIVURQARLADITANYTCVAKNI VARRESAAVI VYVNGGWSTWTEWSV 253  Db 183 GGKLMITYTRKSDAGKYCVGTNMYGERESEVAELTVLERBSFYKRPSNLATVDDSAEF 242  QY 254 -CSASGGGGWQK	288 DRTVSSLLVSVDGSWSPWSKWSACGLDCTHWRSRECSDPAPRNGGEEC : :	Db 357 YQPPQSSRRFSVSQTGDLTITUVQ-RSDVGYYIQTL	OY 449OLTNGHLLSPLGG-GRHTLHHSSPTSEAEEFVSRLSTONY 487  Db 448 LWRKDGVLVSTQDSRIKQLESGVLQIRYAKLGDTGRYTCTASTPSGEA 495  QY 488 FRSLPRGTSNMTYGTFNFLGGRLMIPNTGISLLIPDDAIPRGKIYEIYLTLHKPE- 542  Db 496TWSAYIEVQEFGVPVQPPRPTDPNLIPSAPSKPEV 530

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:

October 4, 2004, 18:11:25; Search time 27 Seconds (without alignments) 1733.743 Million cell updates/sec

US-09-970-944-2 4787 1 MAVRPGLWPALLGIVLAAWL......AVAGLGQPDAGLFTVSEAEC 899 Title: Perfect score: Sequence:

141681 seqs, 52070155 residues BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_42:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	514 homo	homo	mus ก		Q13591 homo sapien	bos t	homo sar	P35448 xenopus lae	m snm 6	pomod	homo	P35441 mus musculu	P07996 homo sapien	P35440 gallus gall	Q28178 bos taurus	P27918 homo sapien	Q64181 cavia porce		Q03696 gallus gall	P98167 bos taurus			Q9esp7 rattus norv	-	homo		075173 homo sapien	oncor	mus m	homo	homo	homo /	5 homo
SUMMARIES	I ID		TSP2 HUMAN	TSP2 MOUSE	SM5A	1 SM5A_HUMAN	TSP2	BAI3		SMSB	BAIZ	SMS	TSP1	TSP	TSP	TSP1_BOVIN	PROP_HUMAN	L PROP_CAVPO	L PROP_MOUSE	NGCA_CHICK	SSPO_BOVIN	L AT14 HUMAN	1 ZO1 HUMAN	1 ATS4 RAT	1 ZO1 MOUSE	1 CO6 HUMAN	1 ATS8 MOUSE	1 ATS4 HUMAN	1 COBB_ONCMY	1 AT15 MOUSE	1 ATS1 HUMAN	1 AT10 HUMAN	1 AT16_HUMAN	1 ATS6 HUMAN
	Query Match Length DB	1584 1									1572	1093	1170	1170	1178																	1077	1224	98
÷	Query Match	.5.	w.	'n.	5.	S	5	δ.	'n.		5.	5.	5	Ŋ.	5	5	4	4	4	3.		m	m M	'n.	'n	m.	ω.	'n.	'n.			3.4		m
	Score	280	273.5	273.5	272.5	270.5	269	267.5	266.5	258.5	258	252	248	246	243.5	243	208.5	205.5	202.5	186	181.5	178.5	175.5	172	170.5	169	167.5	166	162.5	160.5	160.5	160.5	159.5	156.5
	Result No.		7	e	4	Ŋ	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33

Q8te58 homo sapien Q9ukp4 homo sapien	P58397 homo sapien Q8c9w3 m adamts-2	015072 homo sapien Q9wuq1 rattus norv	P97857 mus musculu Q9up79 homo sapien	Q8te56 homo sapien Q9una0 homo sapien	Q98902 fugu rubrip P55314 rattus norv
AT15_HUMAN ATS7_HUMAN	AT12_HUMAN ATS2_MOUSE	ATS3_HUMAN ATS1_RAT	ATS1_MOUSE ATS8_HUMAN	AT17_HUMAN ATS5_HUMAN	CAML_FUGRU COBB_RAT
н н				<b>н н</b>	
950	1593 1213	1205	968	1095	1277 140
3.3	3.2	3.2	3.2	3.2	3.1
156 155	154.5 154	153.5 152	152 151.5	151.5 151	150
34	36	38	40	42	44

## ALIGNMENTS

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rissum=Fibroblast;
                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                                                                                  HUMAN
                                                         361
                                                                                                                                                                                                                                               P35442;
                                                                                                                                                                                                                       TSP2_HUMAN
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INDISPENSABLE FOR INTERACTION WITH BAP1.
N-LINKED (GLCNAC. .) (POTENTIAL).
                              R GO; GO:0005897; C:integral to plasma membrane; TAS.

R GO; GO:0005911; C:intercellular junction; TAS.

R GO; GO:0005911; C:intercellular junction; TAS.

R GO; GO:0007405; F:protein binding; TAS.

R GO; GO:0007405; F:protein binding; TAS.

R GO; GO:0007405; F:cell adhesion; TAS.

R GO; GO:0007425; F:cell adhesion; TAS.

R GO; GO:0007425; F:cell adhesion; TAS.

R GO; GO:0007425; F:peripheral nervous system development; TAS.

R GO; GO:0007425; F:signal transduction; TAS.

R TherPro; IPR001892; GPCR_secretin.

R Fram; PF000182; Promin_receptor.

R Fram; PF000182; FRM 2; 1.

R Fram; PF001825; GPS; 1.

R Fram; PF001825; GPS; 1.

R Fram; PF001825; GPS; 1.

R SWART; SM00189; HormR; 1.

R SWART; SM00209; TSP1; 5.

R PROSITE; PS55021; GPS; 1.

R PROSITE; PS55021; GPS; 1.
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1D (GLCNAC. .) (POTENTIAL).

ED (GLCNAC. .) (POTENTIAL).

ED (GLCNAC. .) (POTENTIAL).

ED (GLCNAC. .) (POTENTIAL).

ED (GLCNAC. .) (POTENTIAL).

(ED (GLCNAC. .) (POTENTIAL).

(ED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                            SMART; SM00209; TSP1, 5.

PROSITE; PS00221; GPS; 1.

PROSITE; PS00649; G_PROTEIN RECEP_F2_1; FALSE NEG.

PROSITE; PS00505; G_PROTEIN RECEP_F2_2; FALSE_NEG.

PROSITE; PS50227; G_PROTEIN RECEP_F2_3; 1.

PROSITE; PS50261; G_PROTEIN RECEP_F2_3; 1.

PROSITE; PS50092; TSP1, 5.

G_PROTEIN COUPLE TS0092; TSP1, 5.

G_PROTEIN COUPLE TS0092; TSP1, 5.

G_PROTEIN COUPLE TS0092; TSP1, 5.
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POLY-PRO.
CELL ATTACHMENT SITE (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DEASF28C77874513 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EXTRACELLULAR (POTENTIAL).
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2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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TYPE-1 3.
TYPE-1 4.
TYPE-1 4.
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1584 AA;
PIR; T00026; T00026
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
309 CNREACGPAGRISSRSQSLRSTDARR---REELGDEL---QQFGFPA-PQTGDPAAE-EW 360
                                                                                                                                                                             468
                                                                      --SPWSVCSTCGEGWQTR-----TRFCVSSSYSTQCSGPLREQRLCNNSAVCPVHG
                                                                                                                                                      411 AWDEWSPWSLCSSTCGRGFRDRTRICR--PPQFGGNPCEGPEKQTKFCNIALCPGRAVDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SECUENCE FROM N.A.
MEDLINE=94010892; PubMed=8406456;
Labell T.L., Byers P.H.;
"Sequence and characterization of the complete human thrombospondin 2 cDNA: potential regulatory role for the 3' untranslated region.";
Genomics 17:225-229(1993).
                                      LRNEDLVDPSLDPNVYITREHSLVVRQARLADTANYTCVAKNIVARRRSASAAVIVYVNG
                                                                                                                             244 GWSTWTEWSVCSASCGRGWQKRSRSCTNPAPLNGGAFCEGQNVHDRTVSSLLV---SVDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    thrombospondin 2.",
J. Biol. Chem. 276:45892-45887(2001).
-- FUNCTION: Adhesive glycoprotein that mediates cell-to-cell and cell-to-matrix interactions. Can bind to fibrinogen, fibronectin, laminin and type V collagen.
-- SUBDIAT: Homotrimer; disulfide-linked.
-- SIMILARITY: Belongs to the thrombospondin family.
-- SIMILARITY: Contains 1 WPC domain.
-- SIMILARITY: Contains 3 EGF-like domains.
-- SIMILARITY: Contains 7 TSP type-1 domains.
-- SIMILARITY: Contains 1 TSP type-1 domains.
-- SIMILARITY: Contains 1 TSP Vive-1 domains.
-- SIMILARITY: Contains 1 TSP Vive-1 domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-92217961; PubMed-1559694; Labell T.L., McGookey Milewicz D.J., Disteche C.M., Byers P.H., "Thrombospondin II: partial CDNA sequence, chromosome location, and expression of a second member of the thrombospondin gene family in
                                                                                                                                                                                                                    301 SWSPWSKWSACGLDCT---HWRSRECSDPAPRNGGEECQGTDLDTRNCTSDLC 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  THROMBOSPONDIN REPEATS DISULFIDE BONDS.
MEDLINE=21588233; PubMed=11590138;
Misenheimer T.M., Hahr A.J., Harms A.C., Annis D.S., Mosher D.F.;
"Disulfide connectivity of recombinant C-terminal region of human
                                                                                                                                                                                                                                               01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                        PRT; 1172 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; L12350; AAA03703.1; -.
EMBL; M81339; -; NOT_ANNOTATED_CDS
PIR; A47379; TSHUP2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 560-1172 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thrombospondin 2 precursor.
THBS2 OR TSP2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       humans.";
Genomics 12:421-429(1992)
                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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10;

Gaps

28;

8; 267

462

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565 -----SSFPDGS-WSCGFCPVGFLGNGTHCEDLDECALVPDICFSTSKVPRCVNTQP 615
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   268 SCTNPAPLNGGAFCEGONVHDRTVSSLLVSVDGSWSPWSKWSACGLDCT---HWRSRECS 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 463 LCNSPVPQMGGKNCKGSGRETKACQGAPCPIDGRWSPWSPWSACTVTCAGGIREKTRVCN 522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DPAPRNGGEECQGTDLDTRNCTSDLCVHSASGPEDVALYVGLIAVAVCLVLLLLVLILVY 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                403 QRGRSCDVTSNTCLGPSIQTRACSLSKCDTRIRQDGGWSHWSPWSSCSVTCGVGNITRIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             209 ROARLADTANYTCVAKNIVARRRSASAA-VIVYVNGGWSTWTEWSVCSASCGRGWOKRSR
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J. Biol. Chem. 266:12821-12824(1991).
-!- FUNCTION: Adhesive glycoprotein that mediates cell-to-cell and cell-to-matrix interactions. Can bind to fibrinogen, fibronectin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=92147683; PubMed=1371115;
Laherty C.D., O'Rourke K., Wolf F.W., Katz R., Seldin M.F.,
Dixit V.M.;
"Characterization of mouse thrombospondin 2 sequence and expression
during cell growth and development.";
J. Biol. Chem. 267:3274-3281(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 1-873 FROM N.A.
MEDLINE=91302287; PubMed=1712771;
Bornstein P., O'Rourke K., Wikstrom K., Wolf F.W., Katz R., Li P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                          GLCNAC...) (POTENTIAL)
(GLCNAC...) (POTENTIAL)
(GLCNAC...) (POTENTIAL)
(GLCNAC...) (POTENTIAL)
(GLCNAC...) (POTENTIAL)
(GLCNAC...) (POTENTIAL)
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129955 MW; 2AC7BB230E44C6F5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                       5.7%; Score 273.5; DB 1;
28.9%; Pred. No. 7.9e-13;
Live 27; Mismatches 110;
                                                                                                                                                                                                       (GLCNAC. .
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AC 003350;
DT 01-JUN-1994 (Rel. 29, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                       N-LINKED (N-LINKED (N-LINK
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                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 28.37
Best Total Similarity 78.37
  740
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858
932
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316
485
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710
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Mus musculus (Mouse).
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316
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TSP TYPE-1 2.
TSP TYPE-1 2.
TSP TYPE-1 3.
EGF-LIKE 1.
EGF-LIKE 3.
TSP TYPE-3 3.
TSP TYPE-3 4.
TSP TYPE-3 5.
TSP TYPE-3 5.
TSP TYPE-3 6.
TSP TYPE-3 7.
TSP TYPE-1 6.
TSP TYPE-1 8.
TSP TY
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PROSITE; PS01086; EGF 2; 1.
PROSITE; PS01086; EGF 3; 2.
PROSITE; PS01092; TST1; 3.
PROSITE; PS01208; WWFC 1; 1.
PROSITE; PS01208; WWFC 1; 1.
PROSITE; PS01208; WWFC 2; 1.
Glycoprotein; Cell adhesion; Calcium-binding; Heparin-binding; Repeat; EGF-like domain; Signal.
SIGNAL
19 1172 THROMBOSPONDIN 2.
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HEPARIN-BINDING (POTENTIAL)
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SIMILARITY
                                                                   GG, GO:0008201; F:heparin binding; TAS.
InterPro; IPR006209; EGF Ca.
InterPro; IPR006209; EGF Like.
InterPro; IPR006209; EGF Iike.
InterPro; IPR008084; TSP1.
InterPro; IPR008085; TSP1.
InterPro; IPR008085; TSP2.
InterPro; IPR008085; TSP2.
InterPro; IPR008085; TSP2.
InterPro; IPR008085; TSPN.
InterPro; IPR008085; TSPN.
InterPro; IPR001007; VWF C.
Pfam; PF00009; EGF; 2.
Pfam; PF00209; TSPN; 1.
Pfam; PF00210; TSPN; 1.
SMART; SM00210; TSPN; 1.
SMART; SM00210; TSPN; 1.

        BY

        BY

HSSP; P00740; 1EDM.
Genew; HGNC:11786; THBS2.
MIM; 188061; -.
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232
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Adams R.H., Betz H., Pueschel A.W.;
"A novel class of murine semaphorins with homology to thrombospondin is differentially expressed during early embryogenesis.";
Mech. Dev. 57:33-45(1996).
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. Mus. NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ch 5.7%; Score 273.5; DB 1; Length 1172; Similarity 36.1%; Pred. No. 7.9e-13; 57; Conservative 22; Mismatches 70; Indels 9;
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30-MAY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Semaphorin 5A precursor (Semaphorin F) (Sema F).
SEMASA OR SEMAF OR SEMF.
Mus musculus (Mouse)
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DR MG1.98746, 1EDM.

MG1.98736, 1EDM.

MG1.98736, 1EDM.

MG1.98736, 1EDM.

DR MG1.98736, 1EDM.

DR MG1.98736, 1EDM.

DR InterPro; 1PR001881; EGF Ca.

DR InterPro; 1PR001861; EGF Ca.

DR InterPro; 1PR001861; TSP1.

DR InterPro; 1PR001861; TSP1.

DR InterPro; 1PR001895, TSP2.

DR InterPro; 1PR001895, TSP2.

DR InterPro; 1PR001895, TSP2.

DR Ffam; PP001009; tsp_1; 3.

DR Pfam; PP001009; tsp_1; 3.

DR Pfam; PP00109; tsp_1; 3.

DR Pfam; PS00109; tsp_1; 3.

DR PRART; SM0011; EGF; 3.

DR SWART; SM0011; EGF; 3.

DR PROSITE; PS00106; EGF 2; 1.

DR PROSITE; PS00108; WPC_1; 1.

DR PROSITE; PS0108; WPC_1; 1.

DR PROSITE; P
                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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TSP TYPE-1 2.
TSP TYPE-1 3.
EGF-LIKE 1.
EGF-LIKE 3.
EGF-LIKE 3.
TSP TYPE-3 1.
TSP TYPE-3 1.
TSP TYPE-3 4.
TSP TYPE-3 5.
TSP TYPE-3 5.
TSP TYPE-3 5.
TSP TYPE-3 6.
TSP TYPE-3 7.
C-TERMINAL.
CELL ATTACHMENT SITE (POTENTIAL).
INTERCHAIN (PROBABLE).
BY SIMILARITY.
laminin and type V collagen.
-!- SUBUNIT: Homotriner; disulfide-linked.
-!- SIMILARITY: Belongs to the thrombospondin family.
-!- SIMILARITY: Contains 1 WWFC domain.
-!- SIMILARITY: Contains 3 EGF-like domains.
-!- SIMILARITY: Contains 3 TSP type-l domains.
-!- SIMILARITY: Contains 7 TSP type-3 domains.
-!- SIMILARITY: Contains 1 TSP N-terminal (TSPN) domain.
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THROMBOSPONDIN 2.
TSP N-TERMINAL.
HEPARIN-BINDING (POTENTIAL)
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EMBL; M64866; AAA40432.1; -.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
  843 VWSCWSSWSKCSATCGGGHYMRTRSCSNPAPAYGGDICLGLHTEEALCNTQTCPESWS 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Simmons A.D., Puschel A.W., McPherson J.D., Overhauser J., Lovett M., "Molecular cloning and mapping of human semaphorin F from the Cri-duchat candidate interval.";
                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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SMART; SM00630; Sema; 1.
SMART; SM00209; TSP1; 6.
PROSITE; PS50092; TSP1; 6.
Signal; Transmembrane; Repeat; Multigene family; Neurogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kalicki J., Harmon G.;
Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
-: FUNCTION: May act as positive axonal guidance cues.
-: SUBCELLULAR LOCATION: Type I membrane protein.
-: SIMILARITY: Belongs to the semaphorin family.
-: SIMILARITY: Contains 1 Sema domain.
-: SIMILARITY: Contains 7 TSP type-I domains.
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30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
28-FRB-2003 (Rel. 41, Last annotation update)
Semaphorin 5A precursor (Semaphorin F) (Sema F).
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PIR; JC5928; JC5928.
Genew; HGMC:10736; SEMASA.
GO:0007155; P:cell adhesion; TAS.
GO; GO:0007267; P:cell-cell signaling; TAS.
GO; GO:0007399; P:neurogenesis; TAS.
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TSP TYPE-1 4.
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InterPro; IPR00165; Plexin-like.
InterPro; IPR00165; Plexin_repeat.
InterPro; IPR000844; TSP1.
InterPro; IPR000804; TSP1.
Pfam; PF01437; PS1; 1.
Pfam; PF01403; Sema; 1.
Pfam; PF00090; tsp1; 6.
PRINTS; PR01705; TSP1REPEAT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1-494 FROM N.A.
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                                                                                                                                        STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-!- FUNCTION: May act as positive axonal guidance cues.
-!- SUBCELIDIAR LOCATION: Type I membrane protein.
-!- TISSUE SPECTFICITY: IN ADULT, DETECTED IN LIVER, BRAIN, KIDNEY, HEART, LUNG AND SPLEEN.
                                                                                                   -!- DEVELOPMENTAL STAGE: DIFFERENTIALLY EXPRESSED IN EMBRYONIC AND ADULT TISSUES. ITS ABUNDANCE DECREASES FROM E10 TO BITH.
-!- SIMILARITY: Belongs to the semaphorin family.
-!- SIMILARITY: Contains 1 Sema domain.
-!- SIMILARITY: Contains 7 TSP type-1 domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R GO; GO:0016021; C:integral to membrane; IDA.

RG; GO:0016021; C:integral to membrane; IDA.

RG; GO:0016041; F:axon guidance receptor activity; IDA.

RG; GO:0010411; P:axon guidance; IMP.

RITERPRO; IPR001565; Plexin_like.

RITERPRO; IPR00165; Plexin_repeat.

RITERPRO; IPR001865; Plexin_repeat.

RITERPRO; IPR001865; TSP.1.

RITERPRO; IPR001865; TSP.1.

REPRO; IPR001865; TSP.1.

REPRO; IPR001865; TSP.1.

REPRO; IPR001865; TSP.1.

REPRO; IPR0176; FSP.1.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEMAPHORIN 5A. EXTRACELLULAR (POTENTIAL)
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Matches 51; Conservative
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TSP TYPE-1 2.
TSP TYPE-1 3.
BGF-LIKE 1.
EGF-LIKE 3.
TSP TYPE-3 1.
TSP TYPE-3 2.
TSP TYPE-3 4.
TSP TYPE-3 4.
TSP TYPE-3 5.
TSP TYPE-3 6.
TSP TYPE-3 6.
TSP TYPE-3 6.
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SWART; SM00209; TSP1; 3.
SWART; SM00209; TSP1; 3.
SWART; SM00210; TSP1; 1.
PROSITE; PS00021; EGF_1; FALSE_NEG.
PROSITE; PS01086; EGF_2; 1.
PROSITE; PS50002; TSP1; 3.
PROSITE; PS50002; TSP1; 3.
PROSITE; PS01208; WWFC_1; 1.
PROSITE; PS0184; WWFC_2; 1.
Glycoprotein; Cell adhesion; Calcium-binding; Repeat; EGF_1ike domain; Signal.
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CELL ATTACHMENT SITE (POTENTIAL).
UNTERCHAIN (PROBABLE).
INTERCHAIN (PROBABLE).
                      SIMILARITY: Contains 1 VWFC domain.
SIMILARITY: Contains 3 EGF-11ke domains.
SIMILARITY: Contains 3 TSP type-1 domains.
SIMILARITY: Contains 7 TSP type-3 domains.
SIMILARITY: Contains 1 TSP N-terminal (TSPN) domain.
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        Belongs to the thrombospondin family.
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InterPro; IPR006209; EGF like.
InterPro; IPR006210; IEGF.
InterPro; IPR006310; IEGF.
InterPro; IPR008085; TSP.1.
InterPro; IPR003367; tsp.3.
InterPro; IPR003367; tsp.3.
InterPro; IPR003129; TSPC.
InterPro; IPR003129; TSPC.
InterPro; IPR00107; VWF.C.
Pfam; PF00008; EGF; 1.
Pfam; PF00412; tsp.3; 13.
Pfam; PF02412; tsp.3; 13.
Pfam; PF02412; tsp.3; 13.
Pfam; PF02412; tsp.3; 13.
Pfam; PF02412; tsp.3; 13.
Pfam; PF00099; vwc; 1.
Pfam; PF00209; vwc; 1.
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      VNGGWSTWIEWSVCSASCGRGWQKRSRSCINPAPLNGGAFCEGQNVHDRTVSSLLVSVDG 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    843 VWSCWSPWTKCSATCGGGHYMRTRSCSNPAPAYGGDICLGLHTBEALCNTQPCPESWS 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     783 VNGAWSAWISWSQCSRDCSRGIRNRKRVCNNPEPKYGGMPCLGPSLEYQECNTLPCPVDG
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Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Adhesive glycoprotein that mediates cell-to-cell and cell-to-matrix interactions. Can bind to fibrinogen, fibronectin, laminin and type V collagen.
-!- SUBUNIT: Homotrimer; disulfide-linked.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Zafar R.S., Moll Y.D., Womack J.F., Walz D.A.;
"Cloning and sequencing of bovine thrombospondin stimulatory effect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Opposite regulation of thrombospondin-1 and corticotropin-induced secreted protein/thrombospondin-2 expression by adrenocorticotropic hormone in adrenocortical cells.";
J. Cell. Physiol. 167:164-172(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TSP2 BOVIN STANDARD; PRT; 1170 AA.
(95116; Q28180;
01-NOV-1997 (Rel. 35, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Thrombospondin 2 precursor (Corticotropin-induced secreted protein)
THBS2 OR TSP2 OR TSP-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinee; Bos.
NCBI_TaxID=9913;
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MEDLINE-96331130; PubMed-8698834;
Lafeuillade B., Pellerin S., Keramidas M., Danik M., Chambaz E.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

Danik M., Chinn A., Lafeuillade M., Keramidas M., Aguesse-Germon
Penhoat A., Chen H., Mosher D., Chambaz E.M., Feige J.J.;
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
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TSP TYPE-1 6.

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42.4%; Pred. No. 1.2e-12;
iive 13; Mismatches 52;
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Best Local Similarity 42.4
Matches 50, Conservative
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Feige J.J.;

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PS50092; TSP1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Fetal brain;
MEDLINE=5819-5217; PubMed=5933023;
MEDLINE=5819-5217; PubMed=5933023;
Shiratsuchi T., Nishimori H., Ichise H., Nakamura Y., Tokino T.;
"Cloning and characterization of BAI2 and BAI3, novel genes homologous to brain-specific angiogenesis inhibitor 1 (BAI1).";
Cytogenet. Cell Genet. 79:103-108(1997).
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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1170 AA;
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InterPro; IPR000884; TSP1.
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InterPro; IPR00107; VWF_C.
Pfam; PP00008; EGF; 2.
Pfam; PP002412; tSP2.
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|TCVSPYGTHCSGPLRESRVCNNTALCPVHGVWEENSPWSLCSFTCGRGQRTRTRSCT--P 374
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                                                                                                                                 TYPE-1 1.
TYPE-1 2.
TYPE-1 3.
TYPE-1 4.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation. the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
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163 EQGIVLPCRPPEGIPPAEVEWLRNEDLVDPSLDPNVYITREHSLVVRQARLADTANYTCV
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R MGD; MGI:107555; Sema5b.
R InterPro; IPR003659; Plexin-like.
R InterPro; IPR003659; Plexin_repeat.
R InterPro; IPR004627; Sema5b.
R InterPro; IPR004627; Sema5.
R InterPro; IPR004684; TSP1.
R Pfam; PF01437; PS1; 1.
R Pfam; PF01437; PS1; 1.
R Pfam; PR01403; Sema; 1.
R Pfam; PR01403; PS1; 1.
SMART; SM00423; PS1; 1.
SMART; SM00209; TSP1; 4.
R SMART; SM00209; TSP1; 5.
R PROSITE; PS50092; TSP1; 5.
R PROSITE; PS50092; TSP1; 5.
R SMART; SM00209; TSP1; 4.
R SMART; SM00209; TSP1; 5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      125 QCVAWSSSGTTKSQKAYIRIARLRKNFEQ-------EPLAKEVSLEQGIVLPC 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       312 OIV-----TRIPGVCLHNGVLHKARDEWTVDSCTECTCONSATICRKVSCP---LMPC 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      171 RP---PEG-----IPPAEVEWLRNEDLVDPSLDPNVYITREHSLVVRQARLADTANY 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  362 TNATIPDGECCPRCWPSDSADDDWSPWSDWTPCS-----VTCGHG-IQQRGRSCDSLAN 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 220 TCVAKNIVAR-----RRSASAAVIVYVNGGWSTWTEWSVCSASCGRGWQKRSRSCTN 271
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30-MAY-2000 (Rel. 39, Last sequence update)
38-MAY-2003 (Rel. 41, Last annotation update)
58-Maphorin 5B precursor (Semaphorin G) (Sema G).
58-MA5B OR SEMAG OR SEMG.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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MW; A9F036D6516C0F24 CRC64;
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Pred. No. 1.9e-11;
0; Mismatches 312; Indels 322;
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PÉRMI, PE01825; GPS; 1.
PÉRMI, PE01825; GPS; 1.
PÉRMI, PE02783; HRM; 1.
PÉRMI, PE00030; LED 1; 4.
SMART; SM00303; GPS; 1.
SMART; SM00008; HOTMR; 1.
SMART; SM00009; TSP1; 4.
PROSITE; PS50221; GPS; 1.
PROSITE; PS50650; GPROTEIN RECEP F2 2; FAIPROSITE; PS50221; GPROTEIN RECEP F2 2; FAIPROSITE; PS50261; GPROTEIN RECEP F2 3; 1.
PROSITE; PS50261; GPROTEIN RECEP F2 3; 1.
PROSITE; PS50261; GPROTEIN RECEP F2 3; 1.
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TISSUBERE Fetal brain;

MEDLINE=9819417; PubMed=9533023;

Shirateuchi T., Nishimori H., Ichise H., Nakamura Y., Tokino T.;

Shirateuchi T., Nishimori H., Ichise H., Nakamura Y., Tokino T.;

Shirateuchi T., Nishimori H., Ichise H., Nakamura Y., Tokino T.;

T "Cloning and characterization of BAI2 and BAI3, novel genes homologous to brain-specific angiogenesis inhibitor I (BAI1).";

Cytogenet. Cell Genet. 79:103:108(1997).

-! FUNCTION: MIGHT BE INVOLVED IN ANGIOGENESIS INHIBITION.

-! FUNCTION: MIGHT BE INVOLVED IN ANGIOGENESIS INHIBITION.

-! SUBCELLULAR LOCATION: Integral membrane protein.

-! SUMILARITY: Contains 4 TSP type-1 domains.
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genes homologous
                                          PEPRINGGLPCVGDAAEYQDCNPQACPVRGAWSCWTAWSQCSASCGGGHYQRTRSCTSPAP
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                               PAPLNGGAFCEGONVHDRTVSSLLVSVDGSWSPWSKWSACGLDC-
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16-OCT-2001 (Rel. 40, Last sequence update)
18-ES-2003 (Rel. 41, Last annotation update)
Exain-specific angiogenesis inhibitor 2 precursor.
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InterPro; IPR001879; hormn receptor.
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Genew; HGNC:944; BAI2.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation — the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modifited and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/amnounce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 VNGGWSTWTEWSVCSASCGRGWQKRSRSCTNPAPLNGGAFCEGQNVHDRTVSSLLVSVDG 300
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Signal; Transmembrane; Repeat; Multigene family; Neurogenesis;
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FUNCTION: May act as positive axonal guidance cues
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                  similarity).
SUBCELLULAR LOCATION: Type I membrane protein.
SUBCERLULAR: Belongs to the semaphorin family.
SIMILARITY: Contains I Sema domain.
SIMILARITY: Contains 7 TSP type-I domains.
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Pred. No. 3.3e-11;
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29.4%; Pred. No. 3...
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Genew; HGNC:10737; SEMA5B.
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InterPro; IPR00165; Plexin-like.
InterPro; IPR001657; Sema.
InterPro; IPR000844; TSP1.
InterPro; IPR0008085; TSP1.
Pfam; PF01437; PS1: 1.
Pfam; PF01403; Sema; 1.
Pfam; PF00090; tsp1: 1.
Pfam; PR01705; TSPIREPEAT.
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SMART; SM00423; PSI; 1.
SMART; SM00630; Sema; 1.
SMART; SM00209; TSPI; 4.
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                                                                                                                ----YVGLIAVAVCL----VLLLLVLILVYCRKKEGLDSDVADSSILTSGFQPVSIKPSKA 415
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  ATCTGALTDTRECSNLECPATDSKWGPWNAWSLCSKTCDTGWQRRFRMCQATGTQGYPCE 501
                                                                                                                                                                                                                                                                         -SRLSTQNYFRSLPRG-----TSNMTYGTFN 504
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Nagase T., Kikuno R., Ishikawa K.-I., Hirosawa M., Ohara O.;
"Prediction of the coding sequences of unidentified human genes. XVII. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro.";
DNA Res. 7:143-150(2000).
                                                                         GTGEEVKPCSEKRCPAFHEMCRDEYVMLMTWKKAAAGEIIYNKCPPNASGSASRRCLLSA
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                    GIDLDTRNCTSDLC -- VHSASGPEDVAL-
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EMBL; M62467; A
EMBL; M62468; F
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M62465;
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                                                                                                                                                                                                                                                                                                                     "Characterization of mouse thrombospondin 2 sequence and expression
                                                                                                                                            Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musimae; Mus.
NCBI_TaxID=10090;
                                     |:| :| :| | 1050
                          409 SIKPSKADNPHLLTIQPDLSTTTTYQGSLCPRQDGPSP-KFQLTNGHLLSP 458
                                                                                                                                                                                                MEDLINE=92128941; PubMed=1774063;
Lawler J., Duquette M., Ferro P., Copeland N.G., Gilbert D.J.,
Jenkins N.A.;
                                                                                                                                                                                                                                                         MEDLINE=92147683; PubMed=1371115;
Laherty C.D., O'Rourke K., Wolf F.W., Katz R., Seldin M.F.,
Dixit V.M.;
BATGCAĞFNLIHLVATGISCFLGSGLITLAVYLSCQHCQRQSQESTL-
                                                                                                                                                                                                                                                                                                                                                                                                          -!- SUBUNIT: Homotrimer; disulfide-linked.
-!- SIMILARITY: Belongs to the thrombospondin family.
-!- SIMILARITY: Contains 1 WWFC domain.
-!- SIMILARITY: Contains 3 EGF-like domains.
-!- SIMILARITY: Contains 3 TSP type-l domains.
-!- SIMILARITY: Contains 1 TSP type-3 domains.
-!- SIMILARITY: Contains 1 TSP N-terminal (TSPN) domain.
                                                                                                                                                                                                                           "Characterization of the murine thrombospondin gene.";
                                                                                                    01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Thrombospondin 1 precursor.
                                                                                      PRT; 1170 AA
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M62451; AAAS0611.1; JOINED.
M62452; AAAS0611.1; JOINED.
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M62454; AAA50611.1;
M62455; AAA50611.1;
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M62457; AAA50611.1;
M62458; AAA50611.1;
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Biol. Chem. 276:6485-6498(2001),
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X14787; CAA32889.1; -.
M14326; AAA61237.1; ALT_SEQ.
M04835; AAA61178.1; -.
M99425; AABS9366.1; -.
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         207 VVRQARLADTANYICVAKNIVAR------RRSASAAVIVYVNGGWSTWTEWSVCSASC 258
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MEDLINE=87057617; PubMed=2430973;
Lawler J., Hynes R.O.
"The structure of human thrombospondin, an adhesive glycoprotein with multiple calcium-binding sites and homologies with several different
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Hennessy S.W., Frazier B.A., Kim D.D., Deckwerth T.L.,
Baumgartel D.M., Rotwein P., Frazier W.A.;
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29.9%; Pred. No. 7.4e-11;
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THBS1 OR TSP1 OR TSP.
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SEQUENCE FROM N.A.
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"Biophysical characterization, including disulfide bond assignments, of the anti-analogenic type I domains of human thrombospondin-1.";

Biochemistry 41:14329-14339 (2002).

"I FUNCTION: Adhesive glycoprotein that mediates cell-to-cell and cell-to-matrix interactions. Can bind to fibrinogen, fibronectin, laminin, type V collagen and integrins alpha-V/beta-1, alpha-V/beta-3 and alpha-IIb/beta-3.

"SIMILARITY: Belongs to the thrombospondin family.

"SIMILARITY: Contains 1 WFC domains.

"SIMILARITY: Contains 3 ESF-like domains.

"SIMILARITY: Contains 3 TSP type-1 domains.

"SIMILARITY: Contains 7 TSP type-3 domains.

"SIMILARITY: Contains 7 TSP type-3 domains.

"SIMILARITY: Contains 1 TSP N-terminal (TSPN) domain.
sites in the 3' untranslated region.";
J. Cell Biol. 108:729-736 (1989).
[3]
SEQUENCE OF 1-397 FROM N.A.
MEDLINE-87157592; PubMed-830396;
Kobayashi S., Eden-Mccutchan F., Framson P., Bornstein P.;
Fantial amino acid sequence of human thrombospondin as determined by analysis of cDNA clones: homology to malarial circumsporozoite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 1-374 FROM N.A.

MEDLINE=86287276; PubMed=3461443;

Dixit V.M., Hennessy S.W., Grant G.A., Rotwein P., Frazier W.A.;

"Characterization of a cDNA encoding the heparin and collagen binding domains of human thrombospondin.";

Proc. Natl. Acad. Sci. U.S.A. 83:5449-5453(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 1-166 FROM N.A.
MEDLINE=89291870; PubMed=2544587;
MEDLINE=89291870; Officeran T.M., Dixit V.M.;
Characterization of the promoter region of the human thrombospondin gene. DNA sequences within the first intron increase transcription.";
J. Biol. Chem. 264:11222-11227(1989).
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TISSUB=Platelet;

TISSUB=21125860; PubMed=11067851;

Hofsteenge J., Huwiler K.G., Macek B., Hess D., Lawler J.,

Mosher D.F., Peter-Katalinic J.;

"C-mannosylation and O-fucosylation of the thrombospondin type 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CARBOHYDRATE-LINKAGE SITES TRP-385; SER-394; TRP-438; TRP-441;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     la Fleur M., Jobin C., Gauthier J., Kreis C.G.;
Submitted (XXX-1992) to the EMBL/GenBank/DDBJ databases.
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207 VVRQARLADTANYTCVAKNIVAR------RRSASAAVIVYVNGGWSTWTEWSVCSASC 258
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                                                                                                                                                                                                                                                                                                                                                                                           452 GDGVITRIRLCNSPSPQMNGKPCEGEARETKACKKDACPINGGWGPWDICSVTCGGG 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=912,7026; PubMed=2022631;
MEDLINE=912,7026; PubMed=2022631;
Lawler J., Duquette M., Ferro P.;
"Cloning and sequencing of chicken thrombospondin.";
J. Biol. Chem. 266:8039-8043(1991).
-!- FUNCTION: Adhesive glycoprotein that mediates cell-to-cell and laminin and type V collagen.
-!- SIMDIAT: Homotrimer; disulfide-linked.
-!- SIMDIAT: Delongs to the thrombospondin family.
-!- SIMILARITY: Contains 1 VWPC domain.
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Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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CHECKAC...) (POTENTIAL).
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N-LINKED (GLCNAC. . .) (POTENTIAL).
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O-LINKED (FUC. .)
/FTId=CAR 000206.
C-LINKED (MAN).
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O-LINKED (FUC. .)
/FTId=CAR 000209.
C-LINKED (MAN).
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01-UUN-1994 (Rel. 29, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
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TSP TYPE-1 2.

TSP TYPE-1 3.

GGF-LIKE 1.

EGF-LIKE 2.

EGF-LIKE 3.

TSP TYPE-3 1.

TSP TYPE-3 1.

TSP TYPE-3 2.

TSP TYPE-3 4.

TSP TYPE-3 4.

TSP TYPE-3 5.

TSP TYPE-3 6.

TSP TYPE-3 6.

TSP TYPE-3 7.

CCLERMINAL.

CCLERMINAL.

CREAT ATTACHMENT SITE (POTENTIAL).

INTERCHAIN (PROBABLE).
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HEPARIN-BINDING (POTENTIAL).
TSP N-TERMINAL.
                                      GO; GO:0004866; R:endopeptidase inhibitor activity; TAS. GO; GO:0004871; F:signal transducer activity; TAS. GO; GO:0007275; P:development; TAS.
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GlycoSuiteDB; P07996; -.
Genew; HGNC:11785; THBS1.
MIM; 188060; -.
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210 OARLADTANYTCVAKNIVARRRS-ASAAVIVYVNGGWSTWTEWSVCSASCGRGWOKRSRS 268
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
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TISSUB-Actric endothelium;
Zafar R.S., Moll Y.D., Weack J.F., Walz D.A.;
Submitted (UNN-1995) to the EMBL/GenBank/DDBJ databases.
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Local Similarity 34.4%; Pred. No. 1.7e-10;
hes 55; Conservative 15; Mismatches 75;
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ID TSP1 BOVIN

AC 028178; Q28179;
DT 01-NOV-1997 (Rel. 35, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Thrombospondin I precursor.

GN THSP1 OR TSP1 OR TSP-1

SO BOS taurus (Bovine).
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                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-!- SIMILARITY: Contains 3 EGF-like domains.
-!- SIMILARITY: Contains 3 TSP type-1 domains.
-!- SIMILARITY: Contains 7 TSP type-3 domains.
-!- SIMILARITY: Contains 1 TSP N-terminal (TSPN) domain.
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DR PTR; SS5501; SS5501;

GlycoSuiteDB; Q28178; -.

DR InterPro; IPR001891; BGF Ca.

InterPro; IPR001891; BGF Ca.

InterPro; IPR000801; BGF Ca.

InterPro; IPR000808; TSP1.

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                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its worlifted and this statement is not removed. Usage by and this statement is not removed. Usage by and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@sib.ch).
-!- FUNCTION: Adhesive glycoprotein that mediates cell-to-cell and cell-to-matrix interactions. Can bind to fibrinogen, fibronectin, laminin, type v collagen and integrins alpha-V/beta-1, alpha-V/beta-3 and alpha-IID/beta-3. May play a role in dentinogenesis and/or maintenance of dentin and dental pulp.
-!- SUBUNIT: Homotrimer; disulfide-linked.
-!- SIBUNIT: Homotrimer; disulfide-linked.
-!- SIMILARITY: Contains 1 VWFC domain.
-!- SIMILARITY: Contains 3 EGF-like domains.
-!- SIMILARITY: Contains 7 TSP type-1 domains.
-!- SIMILARITY: Contains 7 TSP type-3 domains.
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ATTACHMENT SITE (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ^ Match 5.1%; Score 243; DB 1; Length 1170; Local Similarity 30.3%; Pred. No. 1.8e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -> G (IN REF. 2).
ODDGADF3E5FA031A CRC64;
                   INTERCHAIN (PROBABLE) .

BY SIMILARITY.

BY SI
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                                                                                                                                                                                                                                                                                                                    805 80
1170 AA;
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October 4, 2004, 18:21:41; Search time 140 Seconds (without alignments) 2026.078 Million cell updates/sec
                                                                                                                                                                  1 MAVRPGLWPALLGIVLAAWL.....AVAGLGQPDAGLFTVSEAEC 899
                                                                                                                                                                                                                                                                       1017041
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                          1017041 segs, 315518202 residues
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Maximum Match 100%
Listing first 45 summaries
                                                      OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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sp_bacteria:*
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sp_human:*
sp_invertebrate:*
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sp_phage:*
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Maximum DB seq length: 2000000000
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4787
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                                                                                   Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description		Cakis4 mus muscuin	008721 rattus norv	Q96qp4 homo sapien	008747 mus musculu	Oscd16 mus musculu	O7t2z5 gallus gall	O95185 homo sapien	O819t4 xenopus lae	O80y85 mus musculu	Q8kis3 mus musculu	008722 rattus norv	O9d398 mus musculu	OBizjl homo sapien	O86sn3 homo sapien	O8k1s2 mus musculu	Q8wyp7 homo sapien
SUMMARIES		Certs4	008721	Q96GP4	008747	Q8CD16	Q7T2Z5	095185	Q8JGT4	Q80Y85	Q8K1S3	008722	Q9D398	Q81ZJ1	Q86SN3	Q8K1S2	Q8WYP7
DB		7	11	4	11	11	13	4	13	11	11	11	11	4	4	11	4
% Query Match Length DB	100	ם ה	868	544	931	950	931	931	943	1008	945	945	945	934	945	926	948
% Query Match		0.1	95.0	58.9	56.5	56.1	56.0	55.8	53.7	52.3	52.2	52.2	52.1	51.9	51.8	44.8	44.6
Score	7 603 4	10.77	4545.5	2819	2705.5	2686	2679.5	2673.5	2570	2505.5	2499	2497	2493	2486.5	2479	2144.5	2136
Result No.		- •	7	m	4	S	9	7	80	σ	10	11	12	13	14	15	16

↔	drosc caenc caenc	Q8tf26 homo sapien Q96sc3 homo sapien Q96rw7 homo sapien Q811k1 drosophila	Q8iv45 homo sapien Q8cg21 mus musculu Q7tmt3 mus musculu QAcm0 mus musculu		Q7tt33 mus musculu Q8ngw8 homo sapien Q8bve5 mus musculu Q8cgm1 mus musculu Q9tts5 bos taurus Q8cgb2 mus musculu
4 Q8IUTO 11 Q80T71 4 Q8N1Y2 4 Q9H9F3 5 Q9NBL0	5 Q9V7B5 5 Q26262 5 O44171 13 Q9PVD5	4 Q8TF26 4 Q96SC3 4 Q96RW7 5 O8I1K1	4 Q8IV45 11 Q8CG21 11 Q7TMT3	5 Q9UG31 5 Q9VTT0 5 Q7YU67 11 Q80ZF8 5 Q8MYA8	11 Q7TT33 4 Q8NGW8 11 Q8BVE5 11 Q8CGM1 6 Q9TTS5 6 Q8SPM4 11 Q8CGB2
597 328 554 366 1072	1072 947 947 199	351 2673 5636 325	518 1172 1172 1172	1081 1083 1091 1522	1122 1573 478 1560 685 5146
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1597.5 1442 1223.5 971 961.5	956.5 953.5 950.5 694	552.5 366 366 311.5	306 273.5 273.5 271	270.5 269.5 269.5 267 263.5	258.5 258 254.5 24.5 24.5 24.9
17 18 19 20 21	23 24 25 25	22 2 4 6 2 9 8 4 4 6 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	30 32 33	######################################	8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8

## ALIGNMENTS

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RESULT.1

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TO ORKIS4

ORKIS4

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ORKIS4

C 01-0CT-2002 (TrEMBLrel. 22, Created)

DT 01-0CT-2002 (TrEMBLrel. 22, Last sequence update)

DT 01-0CT-2002 (TrEMBLrel. 25, Last annotation update)

DT 01-0CT-2002 (TrEMBLrel. 25, Last annotation update)

DT 01-0CT-2002 (TrEMBLrel. 25, Last annotation update)

DR NOCSHI.

ON WASHILLS (MOUSE).

ON EDNARYCLE, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

ON NOBL TEATLELLOOP,

MAMMALIA; Eutheria; Rodentia; Sciurognathi; Muridae; Musc.

ON NOBL TEATLELLOOP,

RA BEDGINGE FROM N.A.

RA Engelkamp D.;

RY T.Cloning of three mouse unc-5 genes and their expression patterns at RI Shomltted (MAY-2002) to the EMBL/GenBank/DDBJ databases.

DR MAD; MG1894682; Unc5h1.

DR MAD; MG1894682; Unc5h1.

DR MOD; MG1894682; Unc5h1.

DR MOD; MG1894682; Unc5h1.

DR MD; MG1894682; TRRO00481; Death.

DR MD; MG1894682; TRRO00481; TSP1.

DR MTCEPPC; IPRO00481; TSP1.

DR MTCEPPC; IPRO00481; TSP1.

DR MTMS; PRO0047; 19; 1.

DR Ffam; PF00047; 19; 1.

DR SWART; SW00009; DEATH; 1.

DR SWART; SW00019; DEATH; 1.

DR SWART; SW00219; 10]

DR READL; MG1.

DR READL; M
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61 VLLVCKAVPATQIFFKCNGEWVRQVDHVIERSTDSSSGLPTMEVRINVSRQQVEKVFGLE 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 BYWCQCVAWSSSGTTKSQXAYIRIAYLRKNFEQEPLAKEVSLEQGIVLPCRPPEGIPPAE 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 VEWLRNEDLVDPSLDPNVYITREHSLVVRQARLADTANYTCVAKNIVARRRSTSAAVIVY
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                                                                                               Rattus norvegicus (Rat).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
NCBI_TaxID=10116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 11; Length 898;
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01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Transmembrane receptor UNCSHI.
                                                                                                                                                                                                                                                                                                           Κ.,
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BMBL, U87305; AAB57678.1; -
GO; GO:0004912; F:receptor activity; IEA.
GO; GO:0007165; F:receptor activity; IEA.
InterPro; IPR000488; Death.
InterPro; IPR0013599; IG.
InterPro; IPR00110; IG-like.
InterPro; IPR000884; TSP1.
InterPro; IPR000885; TSP1.
InterPro; IPR000906; ZU5.
Pfam; PF00031; death; 1.
                                                                                                                                                                                                                              SEQUENCE FROM N.A.
TISSUEBrain, and Ventral spinal cord;
MEDLINE=97271897; PubMed=9126742;
Tenardo E.D., Hinck L., Masu M., Keino-Masu
Tessier-Lavigne M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 4545.5;
Pred. No. 0;
19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           898 AA; 98840 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PRO1705; TSPIREPEAT.
SWART; SMO0005; DEATH; 1.
SWART; SMO0109; IG; 1.
SWART; SM00209; TSP1; 2.
SWART; SM00218; ZU5; 1.
PROSITE; PSS0835; IG LIKE; 1.
PROSITE; PSS0092; TSP1; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best_Local Similarity 94.7*
Matches 852; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00047; ig; 1.
Pfam; PF00090; tsp_1; 2.
Pfam; PF00791; ZU5; 1.
                                                                                                                                                                                                                                                                                                                                                                                       receptors.
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       PS50092; TSP1; 2.
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                    64 HLLTIQPDLSTTTTTYQGSLCPRQDGPSPKFQLTNGHLLSPLGGGRHTLHHSSPTSEAEE 123
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi; Muridae, Murinae, Mus.
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Rostral cerebellar malformation protein.
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01-JUL-1997 (TrEMBLrel. 04, Created)
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MEDLINE=97271898; PubMed=9126743;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KLHLDSHLSFFASKPSPTAMILNLWEARHFPNGNLSQLAAAVAGLGQPDAGLFTVSEAEC 899
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                                                                                                                                                                                                                                                                                                                        600 WEQDVLHLGEEAPSHLYYCQLEASACYVFTEQLGRFALVGEALSVAAAKRLKLLLFAPVA
                                                                                                                                                                        CTSLEYNIRVYCLHDTHDALKEVVQLEKQLGGQLIQEPRVLHFKDSYHNLRLSIHDVPSS
KPEDVRLPLAGCQTLLSPIVSCGPPGVLLTRPVILAMDHCGEPSPDSWSLRLKKQSCEGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LWKSKLLVSYQEIPFYHIWNGTQRYLHCTFTLERVSPSTSDLACKLWVWQVEGDGQSFSI
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strausberger R.;
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL;
BOOG GOOD STAND 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Similar to transmembrane receptor Unc5H1 (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 2819; DB 4;
Pred. No. 8.2e-252;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58.9%;
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TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
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84 KASPATQIYFKCNSEWVHQKDHVVDERVDETSGLIVREVSIBISRQQVBELFGPEDYWCQ 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     144 CVANSSAGTIKSRKAYVRIAYLRKTFEQEPLGKEVSLEQEVLLQCRPPEGIPVAEVEWLK 203
858 APQTRGHDWRMLAHKLNLDRYLNYFATKSSPTGVILDLWEAQNFPDGNLSMLAAVLEEMG 917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KAVPATQIFFKCNGEWVRQVDHVIERSTDGSSGEPTMEVRINVSRQQVEKVFGLEEYWCQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Team;
annotation
                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

STRAIN-C57BL/6J; TISSUE-Testis;

X The FANTON Consortium,

The FANTON Consortium,

A the RIKEN Genome Exploration Research Group Phase I & II Team

Thandysis of the mouse transcriptome based on functional anno

G0,770 full-length cDNAs.";

I Nature 420:563-573(2002).

R MGD; MGI:1095412; Unc5h3.

R MGD; MGI:1095412; Unc5h3.

R MGD; MGI:1095412; Unc5h3.

R G0; G0:0005042; F:netrin receptor activity; IDA.

R G0; G0:000515; F:protein binding; IDA.

R G0; G0:000515; F:protein binding; IDA.

R G0; G0:000515; F:protein binding; IDA.

R G0; G0:000518; P:protein binding; IDA.

R G0; G0:000519; P:protein binding; IDA.

R InterPro; IPR00110; Ig-like.

R InterPro; IPR00110; Ig-like.

R InterPro; IPR001096; ISP.

R InterPro; IPR001096; ISP.

R InterPro; IPR001096; ISP.

R InterPro; IPR001096; ISP.

R Pfam; PF00090; ISP. 1:

R Pfam; PF
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SMART; SMO0005; DEATH; 1.
SMART; SM00109; IG; 1.
SMART; SM00209; ISP1; 2.
SMART; SM00209; ISP1; 2.
SMART; SM00218; ZUS; 1.
SMART; SM00217E; PSS0092; ISP1; 2.
SMART; SM00217E; PSS0092; TSP1; 2.
                                                                                                                                                                                                                                                                 Created)
Last sequence update)
Last annotation update)
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larity 55.3%; Pred. No. 4.1e-239;
Conservative 153; Mismatches 214;
                                                                                                                                                                                                                    950 AA
                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                              01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, 01-OCT-2003 (TrEMBLrel. 25, Unc5 homolog.
                                                                                                 930
                                                 886 QPDAGLFTVSEAE 898
                                                                                                                                                                                                                 PRELIMINARY;
                                                                                  : : : : : : 918 RHETVVSLAAEGQ
                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse)
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Matches 515;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PDLTSAAAMYRGPVYALHD-VSDKIPMINSPILDPLPNIKIKVYNSSGAVTPQDDLAEFS 498
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                                                                                                                                                                                                                                                                                                                                                                                           26 PAL--ALLSASGTGSAAQDDEFFHELPETFPSDPPEPLPHFLIEPEEAYIVKNKPVNLYC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84 KASPATQIYEKCNSEWVHQKDHVVDERVDETSGLIVREVSIBISRQQVEELFGPEDYWCQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        144 CVAWSSAGTTKSRKAYVRIAYLRKTFEQEPLGKEVSLEQEVLLQCRPPEGIPVAEVEWLK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STWTEWSVCSASCGRGWOKRSRSCTNPAPLNGGAFCEGONVHDRTVSSLLVSVDGSWSPW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STWTEWSVCNSRCGRGYOKRTRTCTNPAPLNGGAFCEGGSV-OKIACTTLCPVDGRWTSW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              383 IVIAVTVCLAITVVVALFVYRROHRDFESDIIDSSALNGGFQPVNIKAARQD---LLAVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    586 SWSLRLKKQSCEGSWEQDVLHLGEEAPSHLYYCQLEASACYVFTEQLGRFALVGEALSVA
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                                                                                                                                                                                                                    8A5D951A4EECA179 CRC64;
Pfam; PP00791; ZU5; 1.
PRINTS; PR01705; TSP!REPEAT.
SWART; SW00005; DEATH; 1.
SWART; SW00209; TSP1; 2.
SWART; SW00219; TSP1; 2.
PROSITE; PS50835; IG_LIKE; 1.
PROSITE; PS50835; IG_LIKE; 1.
PROSITE; PS50082; TSP1; 2.
Immunoglobulin domain.
SEQUENCE 931 AA; 103062 MW; 8P
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Best Local Simil
Matches 515; C
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                                      STWIEWSVCSASCGRGWOKRSRSCINPAPLNGGAFCEGONVHDRTVSSLLVSVDGSWSPW
                                                                                                                 ----SASGPEDVALYVGL-IAVAVCLVLLLLVLILVYCRKKEGLDSDVADSSILTSGF
                                                                                                                            TLHHSS----PISEAEFVSRLS---IQNYF-----RSLPRGT-SNMTYGTFNFL
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NEDLVDPSLDPNVYITREHSLVVRQARLADTANYTCVAKNIVARRSASAAVIVYVNGGW
                                                                                                                                                                          OPVNIKAAROD----LLAVPPDLTSAAAMYRGPVYALHD-VSDKIPMTNSPILDPLPNLKI
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RESULT 7

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                                                                       13; Length
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                          1E23A0D84F2E2C62 CRC64;
                                                                Query Match 56.0%; Score 2679.5; DB 13
Best Local Similarity 56.1%; Pred. No. 1.6e-238;
Matches 511; Conservative 151; Mismatches 218;
EMBL; AY187310; AAO67275.1; -. SEQUENCE 931 AA; 102906 MW;
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                                                                                                                                                                                                                                                                                                        826 PPCRRGADWRTLAQKLHLDSHLSFFASKPSPTAMILNLWEARHFPNGNLSQLAAAVAGLG
                                                                            PDL-STTTTYQGSLCPRQDGPSPKFQLTNGHLLSPLGGGRHTLHHS----SPTSEAREFV
                                                                                                                                                                             SRLS---TQNYF------RSLPRGT--SNMTYGTFNFLGGRLMIPNTGISLLIPPDA
                                                                                                                                                                                                         526 IPRGKIYEIYLTHKPEDVRLPLAGCQTLLSPIVSCGPPGVLLTRPVILAMDHCGEPSPD
                                                                                                                                                                                                                                                                                                                                                                                 586 SWSLRLKKQSCEGSWEQDVLHLGEEAPSHLYYCQLEASACYVFTEQLGRFALVGEALSVA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  646 AAKRLKLLLFAPVACTSLEYNIRVYCLHDTHDALKEVVQLEKQLGGQLIQEPRVLHFKDS
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Anderson R.B., Holt C.E.;
Anderson R.B., Holt C.E.;
Subdited (APR-2002) to the EMBL/GenBank/DDBJ databases.
L. Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
R. Submit, AY099459; AAM14486-1; -.
R. GO; GO:00004872; F:receptor activity; IEA.
R. GO; GO:0007165; P:signal transduction; IEA.
R. InterPro; IPR000488; Death.
R. InterPro; IPR001599; Ig.
R. InterPro; IPR001599; Ig.
R. InterPro; IPR001598; Ig. C2.
R. InterPro; IPR000884; ISP1.
R. InterPro; IPR000884; ISP1.
R. InterPro; IPR000885; TSP1.
R. InterPro; IPR000885; TSP1.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
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Last annotation update)
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Pfam; PF00047; ig; 1.
Pfam; PF00090; tsp_1; 2.
Pfam; PF00791; ZUS; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  322
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PAL--ALLSASGTGSAAQDDDFFHELPETFPSDPPEPLPHFLIEPEEAYIVKNKPVNLYC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9 PALLGIVLAAWLRGSGAQQS---ATVANPVPGANPDLLPHFLVEPEDVYIVKNKPVLLVC
                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                    931 AA
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                                                                                      Created)
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MEDLINE=99000841; PubMed=9782087;
                                                                                                                                                             Transmembrane receptor UNC5C.
                                                                         01-MAY-1999 (TrEMBLrel. 10, 01-MAX-1999 (TrEMBLrel. 10, 01-OCT-2003 (TrEMBLrel. 25,
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Pfam; PF00047; 19; 1.
Pfam; PF00090; tsp 1; 2.
Pfam; PF00791; ZUS; 1.
                                    PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGWSTWTBWSVCSASCGRGWQKRSRSCTNPAPLNGGAFCEGQNVHDRTVSSLLVSVDGSW 302
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                                                                                                                                                                                                                                                                      10 ALLGIVLAAWLRG-----SGAQQSATVANPVPGANPDLLPHFLVEPEDVYIVKNKPVL
                                                                                                                                                                                                                                                                                                                      LVCKAVPATQIFFKCNGEWVRQVDHVIERSTDGSSGEPTMEVRINVSRQQVEKVFGLEEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --ASGPEDVALYVGL-IAVAVCLVLILLVLILVYCRKKEGLDSDVADSS-ILTSGFQPVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   488 YNSSTVGSSPGIHDGNNLLGTKPTGTYPSDNNIMNARNKNMSMQHLLTLPRDSSNSVTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        567 HSCHTLLDQLGTYAFVGESYSRSAIKRLQLAIFAPMLCTSLEYNLKVYCVEDTPDALKEV
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                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                 50;
                                                                                                                                                                                Length 943;
                                                                                                                                                                                                                 Indels
              SWART; SM00409; IG; 2.
SWART; SM00409; IGC2; 1.
SWART; SM00209; TSP1, 2.
SWART; SM00218; ZU5; 1.
PROSITE; PS50835; IG LIKE; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin domain; Receptor.
SEQUENCE 943 AA; 105083 MW; A024E24A7EDB6175 CRC64;
                                                                                                                                                                            Query Match 53.7%; Score 2570; DB 13; Best Local Similarity 52.1%; Pred. No. 2.2e-228; Matches 488; Conservative 166; Mismatches 233;
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GOODSS | PRELIMINARY | RRT; 1008 AA.

CONTROL | WARANEPRORGOLANIAGORACHYGORACE 899

DOODSS | PRELIMINARY | RRT; 1008 AA.

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YIVKNKPVLLVCKAVPATQIFFKCNGEWVRQVDHVIERSTDGSSGEPTMEVRINVSRQQV 113
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                                                                                                                                                                      at
                                                        UNCSH2.

Mus musculus (Mouse).

Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI_TaxID=10090;
                                                                                                                                                                      and their expression patterns
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                                                                                                                                                                                mid-gestation...

Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases. REMBL, AJ487853, CAD32251.1;

REMBL, AJ487853, CAD32251.1;

ROS, GO:0004872; F:receptor activity; IEA.

ROS, GO:0004872; F:receptor activity; IEA.

RINEAPRO; IPR003599; IG.

R InterPro; IPR003599; IG.

R InterPro; IPR003599; IG.

R InterPro; IPR003599; IG.

R InterPro; IPR00884; TSP.1.

R InterPro; IPR008085; TSP.1.

R InterPro; IPR008086; TSP.1.

R InterPro; IPR009096; ZUS.

R Pfam; PF00531; death; 1.
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PROSITE; PS50835; IG LIKE; 1.
PROSITE; PS50835; TSP1, 2.
Immunoglobulin domain; Receptor.
SEQUENCE 945 AA; 103738 MW; 80E896F0F0E06012 CRC64;
Created)
Last sequence update)
Last annotation update)
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                                                                                                                                                          Engelkamp D.;
"Cloning of three mouse unc-5 genes
                                                                                                                                                                                                                                                                                                                                                                                             Pram; Pro0009; 199, 1.
Pfam; Pr00791; 2U5, 1.
Pfam; Pr00791; ZU5, 1.
PRINTS, PR01705; TSPIREPEAT.
SMART; SM00005; DEATH; 1.
SMART; SM00409; IG; 2.
SMART; SM00209; TSP1; 2.
SMART; SM00219; ZU5; 1.
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25,
 (TrEMBLrel. 2 (TrEMBLrel. 2 (TrEMBLrel. 2
                                             Netrin receptor Unc5h2
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 01-OCT-2002
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01-OCT-2003
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                                                                                                                                                                                                                                                                                        SAAVIVYVNGGWSTWTEWSVCSASCGRGWQKRSRSCTNPAPLNGGAFCEGONVHDRTVSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     609 SGTFGCLGGRLSLPGTGVSLLVPNGAIPQGKFYDLYLHINKAEST-LPLSEGSQTVLSPS
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                                                                             EKVFGLEEYWCQCVAWSSSGTTKSQKAYIRIARLRKNFEQEPLAKEVSLEQGIVLPCRPP
                                                           1 MAVRPGLWPALLGIVLAAW----LRG--SGAQQSATVANPVPGANPDLLPHFLVEPEDV
                                                                                                                   YIVKNKPVLLVCKAVPATQIFFKCNGEWVRQVDHVIERSTDGSSGEPTMEVRINVSRQQV
                                  Gaps
  Length 1008
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     DB 11;
    Query Match 52.3%; Score 2505.5; DB 11; Best Local Similarity 52.7%; Pred. No. 2.3e-222; Matches 497; Conservative 153; Mismatches 240;
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
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Leonardo E.D., Hinck L., Masu M., Keino-Masu K., Ackerman S.
Tessier-Lavigne M.;
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01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-JUL-1903 (TrEMBLrel. 25, Last annotation update)
Transmembrane receptor UNC5H2.
Rattus norvegicus (Rat).
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EMBL, 187306; AAB57679.1; -

GO; GO:0004872; F:receptor activity; IEA.

GO; GO:0001465; F:signal transduction; IEA.

InterPro; IPR00110; Ig-like.

InterPro; IPR00110; Ig-like.

InterPro; IPR00888; Ig-C2.

InterPro; IPR00888; TSP1.

InterPro; IPR009086; TSP1.

Pfam; PF00531; death; 1.

Pfam; PF00509; tSP1; 2.

Pfam; PF00791; ZU5; 1.
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SMART; SM00005; DEATH; 1
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SEQUENCE FROM N.A.
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EGVPVAEVEMLKNEDVIDPAQDINFLLITIDHNLIIRQARLSDTANYTCVAKNIVAKRRST
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                                                                                                                                                                                                                                    82;
                                                                                                                                                                                             Length 945;
                                                                                                                                                                                                                                    Indels
                                                                                                                                                  6E9C2A262E560B9B CRC64;
                                                                                                                                                                                    Query Match 52.2%; Score 2497; DB 11; Best Local Similarity 52.0%; Pred. No. 1.3e-221; Matches 501; Conservative 144; Mismatches 236;
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SMART; SM00408; IGC2; 1.
SMART; SM00209; TSP1; 2.
SMART; SM00218; ZUS; 1.
PROSITE; PS50017; DEATH DOMAIN; 1.
PROSITE; PS500835; IG LIKE; 1.
PROSITE; PS50092; TSP1; 2.
Immunoglobulin domain; Receptor.
SEQUENCE 945 AA; 103520 MW; GES
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38 AATVIVYVNGGWSSWAEWSPCSNRCGRGWQKRTRICTNPAPLNGGAFCEGQ-AFQKTACT 296
                                                                                                                                                                                                                                                                                                                                                                   297 TVCPVDGAWTEWSKWSACSTECAHWRSRECMAPPPQNGGRDCSGTLLDSKNCTDGLCVLN 356
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                                                                                                                                                                                                                                  -----HSASGPEDVALYVGL-IAVAVCLVLLLLVLILVYCRKKEGLDSDVADSS-I 400
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                                                                                                                                             114 EKVFGLEEYWCQCVAWSSSGTTKSQKAYIRIARLRKNFEQEPLAKEVSLEQGIVLPCRPP 173
                                                                                                                                                                  294 LLVSVDGSWSPWSKWSACGLDCTHWRSRECSDPAPRNGGEECQGTDLDTRNCTSDLCV-- 351
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476 PLPSLKIKVYNSSTIGSGSGLADGADLLGVLPPGTYPGDF-SRDTHFLHLRSASLGSQHL
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            MAVRPGLWPALLGIVLAAW----LRG--SGAQQSATVANPVPGANPDLLPHFLVEPEDV
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                                                                             YIVKNKPVLLVCKAVPATQIFFKCNGEWVRQVDHVIERSTDGSSGEPTMEVRINVSRQQV
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                                      MRARSGVRSALLLALLLCWDPTPSLAGVDSAGQ----VLPDSYPSAPAEQLPYFLLEPQDA
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Q81ZJ1;
01-MAR-2003 (
01-MAR-2003 (
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SEQUENCE FROM N.A.

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SEQUENCE TISSUE-Medulla oblongata;

MEDILNE-21085660; PubMed-11217851;

RAMAI J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RAMAI J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RAMAI T., Rawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Saito T., Okazai Y., Gojobori T., Bono H., Rasukawa T., Saito R.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Schriml L.M., Grabli F., Suzuki R., Tomita M., Gariboldi M.,

RA Sakai K., Okido T., Fletcher C., Fujita M., Gariboldi M.,

RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Gustincich S., Hill D., Mashima J., Mazararelli J., Mombaerts P.,

RA Gustincich S., Ring B., Ringwald M., Rodriguz I., Sakamcto N.,

RA Sakai H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Havashisaki Y.,
LAOKLHLDSHLSFFASKPSPTAMILNLWEARHFPNGNLSQLAAAVAGLGQPDAGLFTVSE 896
                   Gaps
                                                                                                                                                                                                                                                                                                                    Craniata, Vertebrata, Euteleostomi;
Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hayashizaki Y.; "Functional annotation of a full-length mouse cDNA collection.";
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 409:685-690(2001).

BMBL, AACOMIT', BABAID801, -.

MGD, MGI:894703, Unc5h2.

GO, GO:0007165, P:signal transduction; IEA.

InterPro; IPR00110; I9-like.

InterPro; IPR00110; I9-like.

InterPro; IPR0018598; I9-c2.

InterPro; IPR008685; TSP1.

InterPro; IPR009065; TSP1.
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PROSITE; PSSOU35; IG LIKE; 1.
PROSITE; PSSO092; TSP1; 2.
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Mammalia; Eutheria; Rodentia;
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Pfam; PF00090; tsp 1; 2.
Pfam; PF00791; ZU5; 1.
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SMART; SM00408; IGC2; 1.
SMART; SM00209; TSP1; 2.
SMART; SM00218; ZU5; 1.
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UNC5H2 OR 6330415E02RIK.
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SEQUENCE 945 AA; 10
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597 622 682 716 742

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743 RYLHCTFTLERVSPSTSDLACKLWVWQVEGDGQSFSINFNITKDTRFAELLALESEAG-- 800
                                                                                                                             VQLEKQLGGQLIQEPRVLHFKDSYHNLRLSIHDVPSSLWKSKLLVSYQEIPFYHIWNGTQ
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                                                                                                                                                                                                                                                                                      623 SACYVFTEQLGRFALVGEALSVAAAKRLKLLLFAPVACTSLEYNIRVYCLHDTHDALKEV
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                                                                                                   504 NFLGGRIMIPNTGISLLIPPDAIPRGKIYEIYLTLHKPEDVRLPLA-GCQTLLSPIVSCG
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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A Tanikawa C., Matsuda K., Fukuda S., Nakamura Y., Arakawa H.;
Tanikawa C., Matsuda K., Fukuda S., Nakamura Y., Arakawa H.;
Tanikawa C., Matsuda S., Nakamura Y., Arakawa H.;
Tanikawa C., Matsuda S., Dakuda S., Nakamura Y., Arakawa H.;
Tanikawa C., Matsuda C., Matsuda C., Nat. Cell Biol. 5.216-223(203).

E Mat. PRO004872; F:receptor activity; IEA.

E Mat. Proof 1 PR00186; Death.

E InterPro; IPR00186; Death.

E InterPro; IPR008086; TSP.1.

E InterPro; IPR008086; TSP.1.

E Mat. Pro0030; tsp.1.

E Pfam; Pro0047; ig; 1.

F Pfam; Pro00791; 2015.

E Pfam; PR00791; 2015.

E Pfam; PR00791; 2015.

E Pfam; PR00791; 2015.

E Pfam; PR00791; 1G; 2.

E SMART; SM00408; IG; 2.

E SMART; SM00408; IG; 2.

E SMART; SM00408; IG; 2.
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         T----SEAEEFVSRLSTQNY---
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SMART; SM00209; TSP1; 2.
SMART; SM00218; ZU5; 1.
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                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=22246081; PubMed=12359238;
Komatsuzaki K., Dalvin S., Kinane T.B.;
"Modulation of G(ialpha(2)) signaling by the axonal guidance molecule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KNKPVLLVCKAVPATQIFFKCNGEWVRQVDHVIERSTDGSSGEPTMEVRINVSRQQVEKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 237 VIVYVNGGWSTWIEWSVCSASCGRGWQKRSRSCINPAPLNGGAFCEGQNVHDRTVSSLLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MAVRPGLWPALLGIVLAAW---LRGSGAQQ-SATVANPVPGANPDLLPHFLVEPEDVYIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SVDGSWSPWSKWSACGLDCTHWRSRECSDPAPRNGGEECQGTDLDTRNCTSDLCVHSASG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 4; Length 934;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    255; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        225B3F506D52B780 CRC64;
                                                                                                                                                                                                                                               Biochem. Biophys. Res. Commun. 297:898-905 (2002).
EMBL, AY126437; AAM95701.1; -.
GO: GO:0004872; F:receptor activity; IEA.
GO; GO:000165; P:signal transduction; IEA.
InterPro: IPR000488; Death.
InterPro: IPR00199; Ig.
InterPro: IPR001999; Ig.
InterPro: IPR001999; Ig.
InterPro: IPR001999; Ig.
InterPro: IPR000896; TSP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51.9%; Score 2486.5; DB 4
52.2%; Pred. No. 1.2e-220;
tive 149; Mismatches 255;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Figure 1 Process of Section 1 Process of Section 1 Process of Section 1 Process of Section 1 Process of Section 1 Process of Section 1 Process of Section 1 Process of Section 1 Process of Section 1 Process of Section 1 Process of Section 1 Process of Section 1 Process of Section 1 Process of Section 1 Process of Section 1 Process of Section 1 Process of Section 1 Process of Section 1 Process of Section 1 Process of Section 1 Process of Section 1 Process of Section 1 Process of Section 1 Process of Section 1 Process of Section 1 Process of Section 1 Process of Section 1 Process of Section 1 Process of Section 1 Process of Section 1 Process of Section 1 Process of Section 1 Process of Section 1 Process of Section 1 Process of Section 1 Process of Section 1 Process of Section 1 Process of Section 1 Process of Section 1 Process of Section 1 Process of Section 1 Process of Section 1 Process of Section 1 Process of Section 1 Process of Section 1 Process of Section 1 Process of Section 1 Process of Section 1 Process of Section 1 Process of Section 1 Process of Section 1 Process of Section 1 Process of Section 1 Process of Section 1 Process of Section 1 Process of Section 1 Process of Section 1 Process of Section 1 Process of Section 1 Process of Section 1 Process of Section 1 Process of Section 1 Process of Section 1 Process of Section 1 Process of Section 1 Process of Section 1 Process of Section 1 Process of Section 1 Process of Section 1 Process of Section 1 Process of Section 1 Process of Section 1 Process of Section 1 Process of Section 1 Process of Section 1 Process of Section 1 Process of Section 1 Process of Section 1 Process of Section 1 Process of Section 1 Process of Section 1 Process of Section 1 Process of Section 1 Process of Section 1 Process of Section 1 Process of Section 1 Process of Section 1 Process of Section 1 Process of Section 1 Process of Section 1 Process of Section 1 Process of Section 1 Process of Section 1 Process of Section 1 Process of Section 1 Process of Section 1 Process of Section 1 
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Transmembrane receptor UNC5H2
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SEQUENCE
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GWSSWIEWSACNVRCGRGWQKRSRICTNPAPLNGGAFCEGMSVQKIICTA-LCPVDGSWE 310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COCVAMSSSGTTKSOKAYIRIARLRKNFEQEPLAKEVSLEQGIVLPCRPPEGIPPAEVEW 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64 VCKAVPATQIFFKCNGEWVRQVDHVIERSTDGSSGEPTMEVRINVSRQQVEKVFGLEEYW 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LRNEDLVDPSLDPNVYITREHSLVVRQARLADTANYTCVAKNIVARRRSASAAVIVYVNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPALLGIVLAAWLRGS----GAQQSATVANPVPGANPDLLPHFLVEPEDVYIVKNKPVLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72 RCKARPAMQIFFKCNGEWVHQNEHVSEESLDESSGLKVREVFINVTRQQVEDFHGPEDYW
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                                                                                                                                                                                                                                                                           at
                                                                                                                                                                                                                                                              ingelkamp D.; cloning of three mouse unc-5 genes and their expression patterns
                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PWSKWSACGLDCTHWRSRECSDPAPRNGGEECQGTDLDTRNCTSDLCV-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 11; Length 956;
                                                                                                                                                                                                                                                                                      mid-gestation."

Embil and gestation."

Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.

R EMBL; AJ489184; CAD12252.1; --

R GO; GO: 0004872; F: receptor activity; IEA.

GO; GO: 0004867; F: serine protease inhibitor activity; IEA.

GO; GO: 0007165; P: serine protease inhibitor activity; IEA.

GO; GO: 0007165; P: serine protease inhibitor activity; IEA.

R InterPro; IPR00188; Death.

R InterPro; IPR001989; IG.-2.

R InterPro; IPR00110; IG-1ike.

R InterPro; IPR00110; IG-1ike.

R InterPro; IPR00188; Serpin.

R InterPro; IPR00884; TSP_1.

R InterPro; IPR00884; TSP_1.

R InterPro; IPR009096; ZUS.-

R Pfam; PF00073; death; 1.

R Pfam; PF00791; ZUS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 44.8%; Score 2144.5; DB 11; Lengt
Best Local Similarity 44.8%; Pred. No. 5.9e-189;
Matches 425; Conservative 162; Mismatches 283; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         106351 MW; DFDF07839C10C68D CRC64;
                                                                 Created)
Last sequence update)
Last annotation update)
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                                926
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SWART; SM00409; 105; 1.
SWART; SM00409; 105; 1.
SWART; SM00209; TSP1; 2.
SWART; SM00218; 105; 1.
SWART; SM00218; 105; 1.
PROSITE; PSG0084; SERPIN; 1.
PROSITE; PSG0084; SERPIN; 1.
PROSITE; PSG0092; TSP1; 2.
SEQUENCE 956 AA; 106351 MW; DPI
                                PRT;
                                                                 01-OCT-2002 (TrEMBLrel. 22, 01-OCT-2002 (TrEMBLrel. 22, 01-OCT-2003 (TrEMBLrel. 25,
                                  PRELIMINARY;
                                                                                                                    Netrin receptor Unc5h4 UNC5H4.
                                                                                                                                                       Mus musculus (Mouse)
                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                          NCBI_TaxID=10090;
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RESULT 15
Q8K1S2
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                                                                                                                                                                                                                               61 KNKPVELRCRAFPATQIYFKCNGEWVSQNDHVTQBGLDEATGLRVREVQIEVSRQQVBEL 120
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                                                                                                                                                                                                                                                                               117 FGLEEYWCQCVAWSSSGTTKSQKAYIRIARLRKNFEQEPLAKEVSLEQGIVLPCRPPEGI 176
                                                                                                                                                                                                                                                                                                                                                  177 PPAEVEWLRNEDLVDPSLDPNVYITREHSLVVRQARLADTANYTCVAKNIVARRRSASAA 236
                                                                                                                                                                   GSLDTLCSAPGSTVTTQLGPYAFKIPLSIRQKICNSLDAPNSRGNDWRMLAQKLSMDRYL
                                                                                                                                                                                                                                                                                                                                                                      VIVYVNGGWSTWTEWSVCSASCGRGWQKRSRSCTNPAPLNGGAFCEGQNVHDRTVSSLLV
                                                                                                                                                                                                                                                                                                                                                                                                                                           241 VIVYVNGGWSWAEWSPCSNRCGRGWQKRTRTCTNPAPLNGGAFCEGQ-AFQKTACTTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SVDGSWSPWSKWSACGLDCTHWRSRECSDPAPRNGGEECQGTDLDTRNCTSDLCVHS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PVDGAWTEWSKWSACSTECAHWRSRECWAPPPQNGGRDCSGTLLDSKNCTDGLCMQNKKT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               360 LSDPNSHLLEASG--DAALYAGLVVAIFVVVAILMAVGVVVYRRNCRDFDTDITDSSAAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | || || : | : || || : || || TGGFHPVNFKTARRESNPQLLHPSVPPDLTASAGIYRGPVYALQDS-TDKIFMTNSPLLDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LPSLKVKVYSSSTTGSGPGLADGADLLGVLPPGTYPSDFARDTHFLHLRSASLGSQQLLG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCQTLLSPIVSCGPPGVLLTRPVILAMDHCGEPSPDSWSLRLKKQSCEGSWEQDVLHLGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BAPSHLYYCQLEASACYVFTEQLGRFALVGEALSVAAAKRLKLLLFAPVACTSLEYNIRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QEIPFYHIWNGTQRYLHCTFTLERVSPSTSDLACKLWVWQVEGDGQSFSINFNITKDTRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AELLALESEAG--VPALVGPSAFKIPFLIROKIISSLDPPCRRGADWRTLAOKLHLDSHL
                                                                                                                                                                                                                                                                                                   TSGFOPVSIKPSKADNPHLL--TIQPDLSTTT-TYQGSLCPRQDGPSPKFQLTNGHLLSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YCLHDTHDALKEVVQLEKQLGGQLIQEPRVLHFKDSYHNLRLSIHDVPSSLWKSKLLVSY
                                                                                                                                                                                                             KNKPVLLVCKAVPATQIFFKCNGEWVRQVDHVIERSTDGSSGEPTMEVRINVSRQQVEKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LGGGRHTLHHSSPT----SEAEEFVSRLSTQNY------FRS-----
                                                                                                                                          1 MAVRPGLWPALLGIVLAAW---LRGSGAQQ-SATVANPVPGANPDLLPHFLVEPEDVYIV
                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SFFASKPSPTAMILNLWEARHFPNGNLSQLAAAVAGLGQPDAGLFTVSEAEC 899
                                                                                                       903
                                                                      Length 945;
                                                                                                       Indels
                                  945 AA; 103637 MW; 56064E335F323447 CRC64;
                                                                   51.8%; Score 2479; DB 4; Ilarity 51.8%; Pred. No. 6e-220; Conservative 150; Mismatches 249;
     TSP1; 2.
                                                                      Query Match
Best Local Similarity
Matches 493; Conserv
   PROSITE; PS50092;
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                       Receptor.
SEQUENCE
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371 RWSRRGIENASDIALYSGL-GAAVVAVAVLVIGVTLYRRSHSDYGVDVIDSSALTGGFQT 429
                                                                                                                                                                                                                                         408 VSIKPSKADNPHLL--TIQPDLSTTTTYQGSLCPRQDGPSPKFQLTNGHLLSPLG---- 460
311 VWSEWSVCSPECEHLRIRECTAPPPRNGGKFCEGLSQESENCTDGLCILDKKPLHEIKPQ 370
                                                                                                    ----HSASGPEDVALYVGLIAVAVCLVLLLLVLILVYCRKKEGLDSDVADSSILTSGPQP 407
                                                                                                                                                                                                                                                                                 30 PNFKIVRQGNSLLINPAMQPDLTVSRTYSGPIC-LQD-PLDKELMTESSLFNPLSDIKVK 487
                                                                                                                                                                                                                                                                                                                                                                           -----GGRH----GGRH-----TLHHSSPTSEAEFVSRLSTQNYFR 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     537
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               550 GCQTLLSPIVSCGPPGVLLTRPVILAMDHCGEPSPDSWSLRLKKQSCEGSWEQDVLHLGE 609
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